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<p>(21) International Application Number: PCT/US98/11384</p> <p>(22) International Filing Date: 1 June 1998 (01.06.98)</p> <p>(30) Priority Data: 08/868,373 3 June 1997 (03.06.97) US</p> <p>(71) Applicant (for all designated States except US): CARGILL, INCORPORATED [US/US]; 10547 West McGinty Road, Wayzata, MN 55391 (US).</p> <p>(71)(72) Applicants and Inventors: JAWORSKI, Jan, G. [US/US]; 425 Emerald Woods Drive, Oxford, OH 45058 (US). POST-BEITTENMILLER, Martha, Ann [US/US]; 2375 Quail Road, Ardmore, OH 73491 (US). TODD, James [US/US]; 17 Kelly Drive, Oxford, OH 45056 (US).</p> <p>(74) Agent: LUNDQUIST, Ronald, C.; Fish & Richardson P.C., P.A., Suite 3300, 60 South Sixth Street, Minneapolis, MN 55402 (US).</p>		<p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p>
<p>(54) Title: FATTY ACID ELONGASES</p> <p>(57) Abstract</p> <p>Nucleic acids are disclosed that encode fatty acid β-keto acyl synthases from plants. Such synthases are effective for producing very long chain fatty acids (VLCFA), e.g., C22 to C26, preferentially saturated but also monounsaturated. Also disclosed are polypeptides encoded by such nucleic acids. Transgenic plants expressing these polypeptides exhibit altered levels of VLCFA in one or more tissues, such as seeds or leaves.</p>		

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FATTY ACID ELONGASESField of the Invention

5 This invention relates to fatty acid elongase complexes and nucleic acids encoding elongase proteins. More particularly, the invention relates to nucleic acids encoding β -keto acyl synthase proteins that are effective for producing very long chain fatty acids, polypeptides
10 produced from such nucleic acids and transgenic plants expressing such nucleic acids.

Background of the Invention

Plants are known to synthesize very long chain fatty acids (VLCFAs). VLCFAs are saturated or
15 unsaturated monocarboxylic acids with an unbranched even-numbered carbon chain that is greater than 18 carbons in length. Many VLCFAs are 20-32 carbons in length, but VLCFAs can be up to 60 carbons in length. Important VLCFAs include erucic acid (22:1, i.e., a 22 carbon chain
20 with one double bond), nervonic acid (24:1), behenic acid (22:0), and arachidic acid (20:0).

Plant seeds accumulate mostly 16- and 18-carbon fatty acids. VLCFAs are not desirable in edible oils. Oilseeds of the Crucifereae (e.g., rapeseed) and a few
25 other plants, however, accumulate C20 and C22 fatty acids (FAs). Although plant breeders have developed rapeseed lines that have low levels of VLCFAs for edible oil purposes, even lower levels would be desirable. On the other hand, vegetable oils having elevated levels of
30 VLCFAs are desirable for certain industrial uses, including uses as lubricants, fuels and as a feedstock for plastics, pharmaceuticals and cosmetics.

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The biosynthesis of saturated fatty acids up to an 18-carbon chain occurs in the chloroplast. C2 units from acyl thioesters are linked sequentially, beginning with the condensation of acetyl Coenzyme A (CoA) and malonyl acyl carrier protein (ACP) to form a C4 acyl fatty acid. This condensation reaction is catalyzed by a β -ketoacyl synthase III (KASIII). β -ketoacyl moieties are also referred to as 3-ketoacyl moieties.

The enzyme β -ketoacyl synthase I (KASI) is involved in the addition of C2 groups to form the C6 to C16 saturated fatty acids. KASI catalyzes the stepwise condensation of a fatty acyl moiety (C4 to C14) with malonyl-ACP to produce a 3-ketoacyl-ACP product that is 2 carbons longer than the substrate. The last condensation reaction in the chloroplast, converting C16 to C18, is catalyzed by β -ketoacyl synthase II (KASII).

Each elongation cycle involves three additional enzymatic steps in addition to the condensation reaction as discussed above. Briefly, the β -ketoacyl condensation product is reduced to β -hydroxyacyl-ACP, dehydrated to the enoyl-ACP, and finally reduced to a fully reduced acyl-ACP. The fully reduced fatty acyl-ACP reaction product then serves as the substrate for the next cycle of elongation.

The C18 saturated fatty acid (stearic acid, 18:0) can be transported out of the chloroplast and converted to the monounsaturate C18:1 (oleic acid), and the polyunsaturates C18:2 (linoleic acid) and C18:3 (α -linolenic acid). C18:0 and C18:1 can also be elongated outside the chloroplast to form VLCFAs. The formation of VLCFAs involves the sequential condensation of two carbon groups from malonyl CoA with a C18:0 or C18:1 fatty acid substrate. Elongation of fatty acids longer than 18 carbons depends on the activity of a fatty acid elongase complex to carry out four separate enzyme reactions

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similar to those described above for fatty acid synthesis in the chloroplast. Fehling, Biochem. Biophys. Acta 1082:239-246 (1991). In plants, elongase complexes are distinct from fatty acid synthases since elongases are
5 extraplastidial and membrane bound.

Mutations have been identified in an *Arabidopsis* gene associated with fatty acid elongation. This gene, designated the *FAE1* gene, is involved in the condensation step of an elongation cycle. See, WO 96/13582,
10 incorporated herein by reference. Plants carrying a mutation in *FAE1* have significant decreases in the levels of VLCFAs in seeds. Genes associated with wax biosynthesis in jojoba have also been cloned and sequenced (WO 95/15387, incorporated herein by
15 reference).

Very long chain fatty acids are key components of many biologically important compounds in animals, plants, and microorganisms. For example, in animals, the VLCFA arachidonic acid is a precursor to many prostaglandins.
20 In plants VLCFAs are major constituents of triacylglycerols in many seed oils, are essential precursors for cuticular wax production, and are utilized in the synthesis of glycosylceramides, an important component of the plasma membrane.

25 Obtaining detailed information on the biochemistry of KAS enzymes has been hampered by the difficulties encountered when purifying membrane bound enzymes. Although elongase activities have been partially purified from a number of sources, or studied using cell
30 fractions, the elucidation of the biochemistry of elongase complexes has been hampered by the complexity of the membrane fractions used as the enzyme source. For example, until recently, it was unclear as to whether plant elongase complexes were composed of a
35 multifunctional polypeptide similar to the FAS found in

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animals and yeast, or if the complexes existed as discrete and dissociable enzymes similar to the FAS of plants and bacteria. Partial purification of an elongase KAS, immunoblot identification of the hydroxy acyl
5 dehydrase, and the recent cloning of a KAS gene (*FAE1*) suggest that the enzyme activities of elongase complexes exist on individual enzymes.

Summary of the Invention

The invention disclosed herein relates to an
10 isolated polynucleotide selected from one of the following: SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; an RNA analog of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, or 15; and a polynucleotide having a nucleic acid sequence
15 complementary to one of the above. The polynucleotide can also be a nucleic acid fragment of one of the above sequences that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ
20 ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14.

Also disclosed herein is an isolated polypeptide that has an amino acid sequence substantially identical to one of the following: SEQ ID NO:2, SEQ ID NO:4, SEQ ID
25 NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14. Also disclosed are isolated polynucleotides encoding polypeptides substantially identical in their amino acid sequence to: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID
30 NO:14.

The invention also relates to a transgenic plant containing a nucleic acid construct. The nucleic acid construct comprises a polynucleotide described above. The construct further comprises a regulatory element

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operably linked to the polynucleotide. The regulatory element may a tissue-specific promoter, for example, an epidermal cell-specific promoter or a seed-specific promoter. The regulatory element may be operably linked
5 to the polynucleotide in sense or antisense orientation. The plant has altered levels of very long chain fatty acids in tissues where the polynucleotide is expressed, compared to a parental plant lacking the nucleic acid construct.

10 A method is disclosed for altering the levels of very long chain fatty acids in a plant. The method comprises the steps of creating a nucleic acid construct and introducing the construct into the plant. The construct includes a polynucleotide selected from one of
15 the following: SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; an RNA analog of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, or 15; and a polynucleotide having a nucleic acid sequence complementary to one of the above. The polynucleotide
20 can also be a nucleic acid fragment of one of the above that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ
25 ID NO:14. The polynucleotide is effective for altering the levels of very long chain fatty acids in the plant.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

30 Brief Description of the Drawings

Figure 1 shows the time course of *in vitro* VLCFA synthesis by *FAE1* expressed in yeast, with 3 different acyl-CoA substrates.

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Figure 2 shows the rates of *in vitro* VLCFA synthesis and the VLCFA profiles of *FAE1* expressed in yeast, with 3 different acyl-CoA substrates.

Figure 3 shows the nucleotide sequence of the
5 coding region of the *Arabidopsis* EL1 polynucleotide (SEQ ID NO:1).

Figure 4 shows the deduced amino acid sequence (SEQ ID NO:2) for the EL1 coding sequence of Figure 3.

Figure 5 shows the nucleotide sequence of the
10 coding region of the *Arabidopsis* EL2 polynucleotide (SEQ ID NO:3).

Figure 6 shows the deduced amino acid sequence (SEQ ID NO:4) for the EL2 coding sequence of Figure 5.

Figure 7 shows the nucleotide sequence of the
15 coding region of the *Arabidopsis* EL3 polynucleotide (SEQ ID NO:5).

Figure 8 shows the deduced amino acid sequence (SEQ ID NO:6) for the EL3 coding sequence of Figure 7.

Figure 9 shows the nucleotide sequence of the
20 coding region of the *Arabidopsis* EL4 polynucleotide (SEQ ID NO:7).

Figure 10 shows the deduced amino acid sequence (SEQ ID NO:8) for the EL4 coding sequence of Figure 9.

Figure 11 shows the nucleotide sequence of the
25 coding region of the *Arabidopsis* EL5 polynucleotide (SEQ ID NO:9).

Figure 12 shows the deduced amino acid sequence (SEQ ID NO:10) for the EL5 coding sequence of Figure 11.

Figure 13 shows the nucleotide sequence of the
30 coding region of the *Arabidopsis* EL6 polynucleotide (SEQ ID NO:11).

Figure 14 shows the deduced amino acid sequence (SEQ ID NO:12) for the EL6 coding sequence of Figure 13.

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Figure 15 shows the nucleotide sequence of the coding region of the *Arabidopsis* EL7 polynucleotide (SEQ ID NO:13).

Figure 16 shows the deduced amino acid sequence
5 (SEQ ID NO:14) for the EL7 coding sequence of Figure 15.

Description of the Preferred Embodiments

The present invention comprises isolated nucleic acids (polynucleotides) that encode polypeptides having β -ketoacyl synthase activity. The novel polynucleotides
10 and polypeptides of the invention are involved in the synthesis of very long chain fatty acids and are useful for modulating the total amounts of such fatty acids and the specific VLCFA profile in plants.

A polynucleotide of the invention may be in the
15 form of RNA or in the form of DNA, including cDNA, synthetic DNA or genomic DNA. The DNA may be double-stranded or single-stranded, and if single-stranded, can be either the coding strand or non-coding strand. An RNA analog may be, for example, mRNA or a combination of
20 ribo- and deoxyribonucleotides. Illustrative examples of a polynucleotide of the invention are shown in Figs. 3, 5, 7, 9, 11, 13 and 15.

A polynucleotide of the invention typically is at least 15 nucleotides (or base pairs, bp) in length. In
25 some embodiments, a polynucleotide is about 20 to 100 nucleotides in length, or about 100 to 500 nucleotides in length. In other embodiments, a polynucleotide is greater than about 1500 nucleotides in length and encodes a polypeptide having the amino acid sequence shown in
30 Figs. 4, 6, 8, 10, 12, 14 or 16.

In some embodiments, a polynucleotide of the invention encodes analogs or derivatives of a polypeptide having the deduced amino acid sequence of Figs. 4, 6, 8,

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10, 12, 14 or 16. Such fragments, analogs or derivatives include, for example, naturally occurring allelic variants, non-naturally occurring allelic variants, deletion variants and insertion variants, that do not
5 substantially alter the function of the polypeptide.

A polynucleotide of the invention may further comprise additional nucleic acids. For example, a nucleic acid fragment encoding a secretory or leading amino acid sequence can be fused in-frame to the amino
10 terminal end of one of the EL1 through EL7 polypeptides. Other nucleic acid fragments are known in the art that encode amino acid sequences useful for fusing in-frame to the KAS polypeptides disclosed herein. See, e.g., U.S. 5,629,193 incorporated herein by reference. A
15 polynucleotide may further comprise one or more regulatory elements operably linked to a KAS polynucleotide disclosed herein.

The present invention also comprises polynucleotides that hybridize to a KAS polynucleotide
20 disclosed herein. Such a polynucleotide typically is at least 15 nucleotides in length. Hybridization typically involves Southern analysis (Southern blotting), a method by which the presence of DNA sequences in a target nucleic acid mixture are identified by hybridization to a
25 labeled oligonucleotide or DNA fragment probe. Southern analysis typically involves electrophoretic separation of DNA digests on agarose gels, denaturation of the DNA after electrophoretic separation, and transfer of the DNA to nitrocellulose, nylon, or another suitable membrane
30 support for analysis with a radiolabeled, biotinylated, or enzyme-labeled probe as described in sections 9.37-9.52 of Sambrook et al., (1989) *Molecular Cloning*, second edition, Cold Spring Harbor Laboratory, Plainview; NY.

A polynucleotide can hybridize under moderate
35 stringency conditions or, preferably, under high

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stringency conditions to a KAS polynucleotide disclosed herein. High stringency conditions are used to identify nucleic acids that have a high degree of homology to the probe. High stringency conditions can include the use of

5 low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate (0.1X SSC); 0.1% sodium lauryl sulfate (SDS) at 65°C. Alternatively, a denaturing agent such as formamide can be employed during hybridization, e.g., 50% formamide with 0.1%

10 bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C. Another example is the use of 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium

15 phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC and 0.1% SDS.

Moderate stringency conditions refers to

20 hybridization conditions used to identify nucleic acids that have a lower degree of identity to the probe than do nucleic acids identified under high stringency conditions. Moderate stringency conditions can include the use of higher ionic strength and/or lower

25 temperatures for washing of the hybridization membrane, compared to the ionic strength and temperatures used for high stringency hybridization. For example, a wash solution comprising 0.060 M NaCl/0.0060 M sodium citrate (4X SSC) and 0.1% sodium lauryl sulfate (SDS) can be used

30 at 50°C, with a last wash in 1X SSC, at 65°C. Alternatively, a hybridization wash in 1X SSC at 37°C can be used.

Hybridization can also be done by Northern analysis (Northern blotting), a method used to identify

35 RNAs that hybridize to a known probe such as an

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oligonucleotide, DNA fragment, cDNA or fragment thereof, or RNA fragment. The probe is labeled with a radioisotope such as ^{32}P , by biotinylation or with an enzyme. The RNA to be analyzed can be usually
5 electrophoretically separated on an agarose or polyacrylamide gel, transferred to nitrocellulose, nylon, or other suitable membrane, and hybridized with the probe, using standard techniques well known in the art such as those described in sections 7.39-7.52 of Sambrook
10 et al., *supra*.

A polynucleotide has at least about 70% sequence identity, preferably at least about 80% sequence identity, more preferably at least about 90% sequence identity to SEQ ID NO:1, 3, 5, 7, 9, 11, or 13. Sequence
15 identity can be determined, for example, by computer programs designed to perform single and multiple sequence alignments.

A polynucleotide of the invention can be obtained by chemical synthesis, isolation and cloning from plant
20 genomic DNA or other means known to the art, including the use of PCR technology carried out using oligonucleotides corresponding to portions of SEQ ID NO:1, 3, 5, 7-9, 11 or 13. Polymerase chain reaction (PCR) refers to a procedure or technique in which target
25 nucleic acid is amplified in a manner similar to that described in U.S. Patent No. 4,683,195, incorporated herein by reference, and subsequent modifications of the procedure described therein. Generally, sequence information from the ends of the region of interest or
30 beyond is employed to design oligonucleotide primers that are identical or similar in sequence to opposite strands of the template to be amplified. PCR can be used to amplify specific RNA sequences, specific DNA sequences from total genomic DNA, and cDNA transcribed from total
35 cellular RNA, bacteriophage or plasmid sequences, and the

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like. Alternately, a cDNA library (in an expression vector) can be screened with KAS-specific antibody prepared using peptide sequence(s) from hydrophilic regions of the KAS protein of SEQ ID NO:2 and technology
5 known in the art.

A polypeptide of the invention comprises an isolated polypeptide having the deduced amino acid sequence of Figs. 2, 4, 6, 8, 10 and 12, as well as derivatives and analogs thereof. By "isolated" is meant
10 a polypeptide that is expressed and produced in an environment other than the environment in which the polypeptide is naturally expressed and produced. For example, a plant polypeptide is isolated when expressed and produced in bacteria or fungi. Similarly, a plant
15 polypeptide is isolated when its gene coding sequence is operably linked to a chimeric regulatory element and expressed in a tissue where the polypeptide is not naturally expressed. A polypeptide of the invention also comprises variants of the KAS polypeptides disclosed
20 herein, as discussed above.

A full-length KAS coding sequence may comprise the sequence shown in SEQ ID NO:1, 3, 5, 7, 9, 11 or 13. Alternatively, a chimeric full-length KAS coding sequence may be formed by linking, in-frame, nucleotides from the
25 5' region of a first KAS gene to nucleotides from the 3' region of a second KAS gene, thereby forming a chimeric KAS protein.

It should be appreciated that nucleic acid fragments having a nucleotide sequence other than the KAS
30 sequences disclosed in SEQ ID NO:1, 3, 5, 7, 9, 11 or 13 will encode a polypeptide having the exemplified amino acid coding sequence of SEQ ID NO:2, 4, 6, 8, 10, 12 or 14, respectively. The degeneracy of the genetic code is well-known to the art; i.e., for many amino acids, there

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is more than one nucleotide triplet which serves as the codon for the amino acid.

It should also be appreciated that certain amino acid substitutions can be made in protein sequences without affecting the function of the protein. Generally, conservative amino acid substitutions or substitutions of similar amino acids are tolerated without affecting protein function. Similar amino acids can be those that are similar in size and/or charge properties, for example, aspartate and glutamate and isoleucine and valine are both pairs of similar amino acids. Similarity between amino acid pairs has been assessed in the art in a number of ways. For example, Dayhoff et al. (1978) in *Atlas of Protein Sequence and Structure*, Vol. 5, Suppl. 3, pp. 345-352, which is incorporated by reference herein, provides frequency tables for amino acid substitutions which can be employed as a measure of amino acid similarity.

A nucleic acid construct of the invention comprises a polynucleotide as disclosed herein linked to another, different polynucleotide. For example, a full-length KAS coding sequence may be operably fused in-frame to a nucleic acid fragment that encodes a leader sequence, secretory sequence or other additional amino acid sequences that may be usefully linked to a polypeptide or peptide fragment.

A transgenic plant of the invention contains a nucleic acid construct as described herein. In some embodiments, a transgenic plant contains a nucleic acid construct that comprises a polynucleotide of the invention operably linked to at least one suitable regulatory sequence in sense orientation. Regulatory sequences typically do not themselves code for a gene product. Instead, regulatory sequences affect the expression level of the polynucleotide to which they are

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linked. Examples of regulatory sequences are known in the art and include, without limitation, minimal promoters and promoters of genes preferentially or exclusively expressed in seeds or in epidermal cells of stems and leaves. Native regulatory sequences of the polynucleotides disclosed herein can be readily isolated by those skilled in the art and used in constructs of the invention. Other examples of suitable regulatory sequences include enhancers or enhancer-like elements, introns, 3' non-coding regions such as poly A sequences and other regulatory sequences discussed herein. Molecular biology techniques for preparing such chimeric genes are known in the art.

In other embodiments, a transgenic plant contains a nucleic acid construct comprising a partial or a full-length KAS coding sequence operably linked to at least one suitable regulatory sequence in antisense orientation. The chimeric gene can be introduced into a plant and transgenic progeny displaying expression of the antisense construct are identified.

One may use a polynucleotide disclosed herein for cosuppression as well as for antisense inhibition. Cosuppression of genes in plants may be achieved by expressing, in the sense orientation, the entire or partial coding sequence of a gene. See, e.g., WO 04/11516, incorporated herein by reference.

Transgenic techniques for use in the invention include, without limitation, *Agrobacterium*-mediated transformation, viral vector-mediated transformation, electroporation and particle gun transformation. Illustrative examples of transformation techniques are described in U.S. Patent 5,204,253, (particle gun) and U.S. Patent 5,188,958 (*Agrobacterium*), incorporated herein by reference. Transformation methods utilizing the Ti and Ri plasmids of *Agrobacterium* spp. typically

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use binary-type vectors. Walkerpeach, C. et al., in Plant Molecular Biology Manual, S. Gelvin and R. Schilperoort, eds., Kluwer Dordrecht, C1:1-19 (1994). If cell or tissue cultures are used as the recipient tissue
5 for transformation, plants can be regenerated from transformed cultures by techniques known to those skilled in the art.

Techniques are known for the introduction of DNA into monocots as well as dicots, as are the techniques
10 for culturing such plant tissues and regenerating those tissues. Monocots which have been successfully transformed and regenerated include wheat, corn, rye, rice, and asparagus. See, e.g., U.S. Patent Nos. 5,484,956 and 5,550,318, incorporated herein by
15 reference.

For efficient production of transgenic plants from plant cells, it is desirable that the plant tissue used for transformation possess a high capacity for regeneration. Transgenic plants of woody species such as
20 poplar and aspen have also been obtained. Technology is also available for the manipulation, transformation, and regeneration of gymnosperm plants. For example, U.S. Patent No. 5,122,466 describes the biolistic transformation of conifers, with preferred target tissue
25 being meristematic and cotyledon and hypocotyl tissues. U.S. Patent No. 5,041,382 describes enrichment of conifer embryonal cells.

Seeds produced by a transgenic plant(s) can be grown and then selfed (or outcrossed and selfed) to
30 obtain seeds homozygous for the construct. Seeds can be analyzed in order to identify those homozygotes having the desired expression of the construct. Transgenic plants may be entered into a breeding program, e.g., to introgress the novel construct into other lines, to
35 transfer the construct to other species, or for further

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selection of other desirable traits. Alternatively, transgenic plants may be propagated vegetatively for those species amenable to such techniques. A nucleic acid construct of the invention can alter the levels of
5 very long chain fatty acids in plant tissues expressing the polynucleotide, compared to VLCFA levels in corresponding tissues from an otherwise identical plant not expressing the polynucleotide. A comparison can be made, for example, between a non-transgenic plant of a
10 plant line and a transgenic plant of the same plant line. Levels of VLCFAs having 20-32 carbons and/or levels of VLCFAs having 32-60 carbons can be altered in plants disclosed herein. Plants having an altered VLCFA composition may be identified by techniques known to the
15 skilled artisan, e.g., thin layer chromatography or gas-liquid chromatography (GLC) analysis of the appropriate plant tissue.

A suitable group of plants with which to practice the invention are the *Brassica* species, including *B.*
20 *napus*, *B. rapa*, *B. juncea*, and *B. hirta*. Other suitable plants include, without limitation, soybean (*Glycine max*), sunflower (*Helianthus annuus*) and corn (*Zea mays*).

A method according to the invention comprises introducing a nucleic acid construct into a plant cell
25 and producing a plant (as well as progeny of such a plant) from the transformed cell. Progeny includes descendants of a particular plant or plant line, e.g., seeds developed on an instant plant are descendants. Progeny of an instant plant include seeds formed on F_1 ,
30 F_2 , F_3 , and subsequent generation plants, or seeds formed on BC_1 , BC_2 , BC_3 , and subsequent generation plants.

Methods and compositions according to the invention are useful in that the resulting plants and plant lines have desirable alterations in very long chain
35 fatty acid composition. Suitable tissues in which to

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express polynucleotides and/or polypeptides of the invention include, without limitation, seeds, stems and leaves. Leaf tissues of interest include cells and tissues of the epidermis, e.g., cells that are involved
5 in forming trichomes. Of particular interest are epidermal cells involved in forming the cuticular layer. The cuticular layer comprises various very long chain fatty acids and VLCFA derivatives such as alkanes, esters, alcohols and aldehydes. Altering the composition
10 and amount of VLCFAs in epidermal cells and tissues may enhance defense mechanisms and drought tolerance of plants disclosed herein.

Polynucleotides of the invention can be used as markers in plant genetic mapping and plant breeding
15 programs. Such markers may include RFLP, RAPD, or PCR markers, for example. Marker-assisted breeding techniques may be used to identify and follow a desired fatty acid composition during the breeding process. Marker-assisted breeding techniques may be used in
20 addition to, or as an alternative to, other sorts of identification techniques. An example of marker-assisted breeding is the use of PCR primers that specifically amplify a sequence from a desired KAS that has been introduced into a plant line and is being crossed into
25 other plant lines.

Plants and plant lines disclosed herein preferably have superior agronomic properties. Superior agronomic characteristics include, for example, increased seed germination percentage, increased seedling vigor,
30 increased resistance to seedling fungal diseases (damping off, root rot and the like), increased yield, and improved standability.

While the invention is susceptible to various modifications and alternative forms, certain specific
35 embodiments thereof are described in the general methods

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and examples set forth below. It should be understood, however, that these examples are not intended to limit the invention to the particular forms disclosed but, instead the invention is to cover all modifications, 5 equivalents and alternatives falling within the scope of the invention.

EXAMPLES

Example 1

Cloning and Expression of FAE1 in Yeast Cells

10 The open reading frame of the *Arabidopsis FAE1* gene was amplified directly by PCR, using *Arabidopsis thaliana* cv. Columbia genomic DNA as a template, pfu DNA polymerase and the following primers:

5'-CTCGAGGAGCAATGACGTCCGTTAA-3' and 5'-

15 CTCGAGTTAGGACCGACCGTTTGTG-3'. The PCR product was blunt-end cloned into the *Eco* RV site of pBluescript (Stratagene, La Jolla, CA),

 The *FAE1* gene was excised from the Bluescript vector with *Bam*HI, and then subcloned into the pYEura3 20 (Clontech, Palo Alto, CA). pYEura3 is a yeast centromere-containing, episomal plasmid that is propagated stably through cell division. The *FAE1* gene was inserted downstream of a *GAL1* promoter in pYEura3. The *GAL1* promoter is induced when galactose is present in 25 the medium and repressed when glucose is present in the growth medium.

 Insertion of the *FAE1* gene in the sense orientation was confirmed by PCR, and pYEura3/*FAE1* was used to transform *Saccharomyces cerevisiae* strain AB1380 30 using a lithium acetate procedure as described in Gietz, R. and Woods, R., in *Molecular Genetics of Yeast: Practical Approaches*, Oxford Press, pp. 121-134 (1994). Plasmid DNA was isolated from putative transformants, and

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the presence of the *FAE1*/pYEUra3 construct was confirmed by Southern analysis.

Yeast transformed with pYEUra3 having *FAE1* operably linked to the *GAL1* promoter were grown in the presence of galactose or glucose and were analyzed for the expression of *FAE1*. As a control, yeast transformed with pYEUra3 containing no insert were also assayed. Analysis of such control preparations yielded fatty acid compositions and fatty acid elongation rates similar to those of yeast transformed with pYEUra3/*FAE1* and grown with glucose as the carbon source.

The fatty acid composition of yeast cells grown in the presence of galactose was compared to that of cells grown in the presence of glucose, to determine if VLCFA were found in the galactose-induced cells.

Transformed yeast cells were grown overnight in YPD media at 30°C with vigorous shaking. One hundred μ l of the overnight culture were used to inoculate 40 ml of complete minimal uracil dropout media (CM-Ura) supplemented with either glucose or galactose (2% w/v). Cultures were grown at 30°C to an OD₆₀₀ of approximately 1.3 to 1.5. Cells were harvested by centrifugation at 5000 Xg for 10 min. Total lipids were extracted from the cells with 2 volumes of 4N KOH in 100% methanol for 60 min. at 80°C. Fatty acids were saponified and methyl esters were prepared by drying the samples and resuspending in 0.5 ml of boron trichloride in methanol (10% v/v). Samples were incubated at 50°C for 15 min in a sealed tube. About 2 ml of water was then added and the fatty methyl esters were extracted thrice with 1 ml of hexane. Extracts were dried under nitrogen and redissolved in hexane. See Hlousek-Radojcic, A. et al., Plant J. 8:803-809. Methyl esters were analyzed on an HP 5890 series II gas chromatograph equipped with a 5771MSD and 7673 auto injector (Hewlett-Packard, Cincinnati, OH).

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Methyl esters were separated on a DB-23 (J&W Scientific) capillary column (30 m X 0.25 mm X 0.25 μ m). The column was operated with helium carrier gas and splitless injection (injection temperature 280°C, detector temperature 280°C). After an initial 3 min. at 100°C, the oven temperature was raised to 250° at 20°C min⁻¹ and maintained at that temperature for an additional 3 min. The identity of the peaks was verified by cochromatography with authentic standards and by mass spectrometer analysis.

The results clearly revealed the appearance of both 20:1 and 22:1 acyl-CoA products in galactose-induced yeast containing the *FAE1* coding sequence. Uninduced yeast cells failed to accumulated significant amounts of fatty acids longer than C18. These results indicate that expression of *FAE1* in yeast resulted in functional KAS activity and functional elongase activity.

Example 2

***FAE1* Activity in Yeast Microsomes**

The functional expression of the *FAE1* KAS was analyzed by isolating microsomes from transformed yeast cells and assaying these microsomes *in vitro* for elongase activity.

Transformed yeast cells were grown in the presence of either glucose or galactose (2% w/v) as described in Example 1. Cells were harvested by centrifugation at 5000 Xg for 10 min and washed with 10 ml ice cold isolation buffer (IB), which contains 80 mM Hepes-KOH, pH 7.2, 5 mM EGTA, 5 mM EDTA, 10 mM KCl, 320 mM sucrose and 2 mM DTT). Cells were then resuspended in enough IB to fill a 1.7 ml tube containing 700 μ l of 0.5 μ m glass beads and yeast microsomes were isolated from the cells essentially as described in Tillman, T. and Bell, R., J. Biol. Chem. 261:9144-9149 (1986). The microsomal

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membrane pellet was recovered by centrifugation at 252,000 xg for 60 min. The pellet was rinsed by resuspending in 40 ml fresh IB and again recovered by centrifugation at 252000 Xg for 60 min. Microsomal
5 pellets were resuspended in a minimal volume of IB, and the protein concentration adjusted to $2.5 \mu\text{g } \mu\text{l}^{-1}$ by addition of IB containing 15% glycerol. Microsomes were frozen on dry ice and stored at -80°C . The protein concentration in microsomes was determined by the
10 Bradford method (Bradford, 1976).

Fatty acid elongase activity was measured essentially as described in Hlousek-Radojcic, A. et al., Plant J. 8:803-809 (1995). Briefly, the standard elongation reaction mix contained 80 mM Hepes-KOH, pH
15 7.2, 20 mM MgCl_2 , 500 μM NADPH, 1 mM ATP, 100 uM malonyl-CoA, 10 μM CoA-SH and 15 μM radioactive acyl-CoA substrate. The radiolabeled substrate was either $[1\text{-}^{14}\text{C}]18:1\text{-CoA}$ (50 uCi μmol^{-1}), $[1\text{-}^{14}\text{C}]18:0\text{-CoA}$ (55 uCi μmol^{-1}), or $[1\text{-}^{14}\text{C}]16:0\text{-CoA}$ (54 uCi μmol^{-1}). The reaction was
20 initiated by the addition of yeast microsomes (5 μg protein) and the mixture incubated at 30°C for the indicated period of time. The final reaction volume was 25 μl .

Methyl esters of the acyl-CoA elongation products
25 were prepared as described in Example 1. Methyl esters were separated on reversed phase silica gel KC18 TLC plates (Whatman, 250 uM thick), quantified by phosphorimaging, and analyzed on by ImageQuant software (Molecular Dynamics, Inc., Sunnyvale, CA). The detection
30 limit for each product is about 0.001 nanomoles per min. per mg microsomal protein, depending on the phosphorimage exposure time.

Results of representative *in vitro* elongation assays are shown in Figs. 1 and 2. The results indicate
35 that microsomes from galactose-induced cells expressing

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FAE1 catalyzed multiple cycles of elongation starting with either C16:0 acyl CoA, C18:0 acyl CoA, or C18:1 acyl-CoA as the substrate (Fig. 1). The 16:0 and 18:0 acyl-CoA substrates were elongated to C26:0 acyl-CoA. In contrast, the 18:1-CoA substrate was elongated primarily to C20:1, with only low levels of C22:1 acyl-CoA being produced. Occasionally, trace levels of C24:1 CoA were also observed. Although the chain length of the products from the 18:1 acyl-CoA substrate were less than the chain length from the saturated acyl-CoA substrates, the rate of elongation of oleoyl-CoA was about 2- and 3-fold higher than the rates of elongation of 16:0-CoA and 18:0-CoA, respectively.

The elongation activity observed in microsomes from uninduced cells indicated that there was a low level of endogenous elongase activity when 18:1-CoA or 18:0-CoA were used as substrates. There was substantial 16:0-CoA elongase activity (10.1 nmol mg protein⁻¹ at 30 min) in microsomes from uninduced cells (Fig. 2). However, the major product of 16:0 elongation using uninduced microsomes was C18:0 acyl CoA, with only small amounts of products beyond this length. The elongation of the 16:0 acyl-CoA substrate presumably is due to an endogenous yeast elongase.

Elongation of 18:1 CoA by microsomes from induced cells occurred at a rate about 18-fold higher than in microsomes isolated from the uninduced cells (Fig. 2). With microsomes from induced yeast, synthesis of 20:0 CoA from the 16:0 CoA substrate, occurred at a rate similar to that seen when the substrate was 18:0 CoA (4.2 vs. 5.1 nmol mg protein⁻¹). The total rate of elongation of [¹⁴C] 16:0-CoA by microsomes from induced cells (15.8 nmol mg protein⁻¹ at 30 min.) was more than 50% higher than elongation of [¹⁴C] 16:0-CoA by microsomes from uninduced cells, suggesting that the *FAE1* KAS utilized 16:0-CoA as

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a substrate in addition to C18-C24 acyl-CoAs. The *FAE1* elongase KAS activity, i.e., the difference in the 16:0 elongation rates between microsomes from induced and uninduced cells, was 5.7 nmol mg protein⁻¹. The
5 elongation rate with the 16:0 substrate thus was similar to the elongase activity of the *FAE1* elongase KAS with the 18:0 substrate.

These results indicate that *FAE1* KAS expressed in yeast could synthesize 3-ketoacyl-CoA *in vitro* and, in
10 combination with yeast reductases and dehydrases, could form a functional VLCFA elongase complex. In addition, these results suggest that *FAE1* is membrane-bound in yeast cells.

Example 3

15 **Cloning and Sequencing of *Arabidopsis* Elongase Genes**

The sequence of a jojoba seed cDNA (see WO 93/10241 and WO 95/15387, incorporated herein by reference) was used to search the *Arabidopsis* expressed sequence tag (EST) database of the *Arabidopsis* Genome
20 Stock Center (The Ohio State University, Columbus, Ohio). The BLAST computer program (National Institutes of Health, Bethesda, MD, USA) was used to perform the search. The search identified two ESTs (ATTS1282 and ATTS3218) that had a high degree of sequence identity
25 with the jojoba sequence. The ATTS1282 and ATTS3218 ESTs appeared to be partial cDNA clones rather than full-length clones based on the length of the jojoba sequence.

A genomic DNA library from *Arabidopsis thaliana* cv. Columbia, was prepared in the lambda GEM11 vector
30 (Promega, Madison, Wisconsin) and was obtained from Ron Davis, Stanford University, Stanford, CA. The library was hybridized with ATTS1282 and ATTS3218 as probes and 2 clones were identified for each EST. Phage DNA was isolated from each of the hybridizing clones, the genomic

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insert was excised with the restriction enzyme Sac I and subcloned into the plasmid pBluescript (Stratagene, La Jolla, CA). One clone from the ATTS1282 hybridization was designated EL1 and one clone from the ATTS3218

5 hybridization was designated EL2.

A yeast expression library, containing cDNA from *Arabidopsis thaliana* cv. Columbia, was prepared in the lambda YES expression vector described in Elledge et al. (Elledge, S. et al., Proc. Natl. Acad. Sci USA 88:1731-
10 1735 (1991) and was obtained from Ron Davis at Stanford University, Stanford, CA. The library was hybridized with a EL2 partial cDNA probe. A full-length EL2 cDNA was not identified. However, the probe did identify a full-length cDNA which was designated EL3.

15 A consensus sequence for the C-terminal region of EL1, EL2 and the jojoba cDNA polypeptides was identified by sequence alignment using DNA analysis programs from DNASTar, Madison, Wisconsin. This consensus sequence was used to search the *Arabidopsis* EST database again for β -
20 keto acyl synthase sequences. These searches identified four additional putative β -keto acyl synthase ESTs, which were designated EL4 through EL7. EL4, EL5, EL6, and EL7 have homology to Genbank Accession Nos. T04345, T44939, T22193 and T76700, respectively.

25 The lambda YES cDNA expression library described above was hybridized with the EL1 and EL4-EL7 ESTs as probes. This screen identified full-length cDNAs for EL1, EL5 and EL6.

The lambda GEM11 genomic library was hybridized
30 with the EL4 and EL7 ESTs as probes. This screen identified full-length genomic clones for EL4 and EL7. Phage DNA was isolated from each of the hybridizing clones and subcloned into pBluescript as described above.

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The 7 EL clones were sequenced on both strands with regions of overlap for each sequence run.

Sequencing was carried out with an ABI automated sequencer (Applied Biosystems, Inc., Foster City, California), following the manufacturer's instructions.

The nucleotide sequences for the coding regions of EL1-EL7 are shown in Figs. 3, 5, 7, 9, 11, 13 and 15, respectively. The deduced amino acid sequences for EL1-EL7 are shown in Figs. 4, 6, 8, 10, 12, 14 and 16, respectively, using the standard one-letter amino acid code. The EL1, EL2 and EL7 genomic clones appeared to lack introns. The EL4 genomic clone contained one intron near the 5' end of the coding region.

The nucleotide sequences of the 7 EL polynucleotides were compared to 5 DNA sequences present in Genbank. Genbank, National Center for Biotechnology Information, Bethesda, MD. Two of the 5 accessions were cloned from members of the Brassicaceae: the *Arabidopsis* FAE1 sequence (Accession U29142) and a *Brassica napus* sequence (Accession U50771). Three of the accessions were cloned from jojoba (*Simmondsia chinensis*): 2 wax biosynthesis genes (Accessions I14084 and I14085) and a jojoba KAS gene (Accession U37088). See also U.S. Patent 5,445,947, incorporated herein by reference.

Multiple alignment of the 12 sequences was carried out with a computer program sold under the trade name MEGALIGN Lasergene by DNASTar (Madison, Wisconsin). Alignments were done using the Clustal method with weighted residue weight table. The nucleotide sequence similarity index and percent divergence based on the multiple alignment algorithm is shown in Table 1. The nucleotide sequences of EL1-EL7 are distinguishable from the 5 DNA sequences obtained from Genbank.

The deduced amino acid sequences of the EL1-7 polypeptides were compared with the MEGALIGN program to

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the deduced amino acid sequences of the same 5 Genbank clones, using the Clustal method with PAM250 residue weight table. The amino acid sequence similarity and percent divergence are shown in Table 2. The amino acid
5 sequences of EL1-EL7 polypeptides are distinguishable from those of the Genbank sequences.

	1	2	3	4	5	6	7	8	9	10	11	12	
1		77.5	62.4	58.8	57.0	54.9	47.0	42.8	42.9	43.1	44.7	41.3	1
2	18.1		61.0	57.9	55.4	53.7	46.9	42.7	44.1	42.9	42.3	40.5	2
3	40.4	41.0		70.5	59.3	56.4	46.7	48.5	48.1	48.6	46.5	43.5	3
4	43.9	44.3	28.0		56.3	55.4	46.5	47.0	45.1	47.2	47.4	42.3	4
5	40.7	42.3	45.0	45.0		68.0	54.0	46.8	46.6	46.4	49.0	47.2	5
6	45.8	48.9	46.0	47.3	32.4		53.6	48.6	48.2	48.6	49.0	49.2	6
7	74.1	71.0	69.4	67.3	64.3	64.5		49.8	49.2	49.8	47.7	48.2	7
8	68.1	66.2	63.4	63.1	65.5	64.2	56.1		97.7	99.7	48.4	45.8	8
9	67.0	65.4	63.7	64.6	64.6	64.1	56.6	1.1		95.9	47.6	44.8	9
10	67.2	65.2	61.8	61.4	64.1	63.0	56.3	0.2	1.1		48.4	45.3	10
11	88.6	85.8	81.0	77.0	77.4	82.4	83.1	71.1	71.1	69.9		48.3	11
12	95.7	90.4	95.4	91.5	84.5	82.8	91.9	73.4	73.8	73.3	59.9		12
	1	2	3	4	5	6	7	8	9	10	11	12	

TABLE 2

Amino acid sequence pair distances of EL1-EL7, using Clustal method with PAM250 residue weight table.

	1	2	3	4	5	6	7	8	9	10	11	12	
1		72.0	62.9	59.8	60.9	60.2	50.3	51.9	52.1	51.5	49.1	42.0	1
2	31.1		60.1	57.5	58.7	57.1	49.8	49.8	50.0	49.2	49.6	44.4	2
3	47.4	48.7		82.4	60.7	63.0	50.0	51.4	51.6	50.8	47.8	43.9	3
4	51.8	52.8	17.9		60.2	61.0	49.2	50.3	50.5	49.7	46.5	42.4	4
5	49.0	51.3	45.8	46.2		75.8	61.0	58.7	58.9	58.3	55.0	55.6	5
6	52.6	55.5	42.8	46.5	29.3		61.8	55.7	55.7	54.9	52.9	50.5	6
7	74.7	70.5	71.8	74.4	52.0	50.8		52.8	52.8	51.8	53.4	51.6	7
8	66.7	69.2	66.2	67.3	54.8	59.8	67.7		99.8	96.9	53.1	52.0	8
9	66.3	68.7	66.2	67.3	54.0	59.3	67.7	0.2		96.9	53.1	51.9	9
10	66.3	69.7	66.6	67.8	54.5	60.7	68.6	1.8	1.6		51.7	50.7	10
11	73.6	73.7	72.8	74.4	60.8	66.0	67.2	63.9	63.9	65.3		50.8	11
12	84.8	85.5	82.7	83.3	60.6	70.8	67.1	68.5	68.5	69.9	69.4		12
	1	2	3	4	5	6	7	8	9	10	11	12	

EL2

EL3

ATPAE1 U29142

BNFAE1 U50771

EL7

EL5

EL6

JQJKCS U37088

JKCS11 I14085

JKCS10 I14084

EL1

EL4

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Example 4**Expression of EL1 and EL2 in Yeast**

The open reading frames (ORFs) for the EL2, EL4 and EL7 clones were amplified by PCR. The EL2 ORF was cloned into λ YES using the primers: CTCGAGCAAGTCCACTACCACGCA and CTCGAGCGAGTCAGAAGGAACAAA. The EL4 ORF was cloned into pYEura3 using the primers: GATAATTTAGAGAGGCACAGGGT and GTCGACACAAGAATGGGTAGATCCAA. The EL7 ORF was cloned into pYEura3 using the primers: CAGTTCCTCAAACGAAGCTA and GTCGACTTCTCAATGGACGGTGCCGGA. Amplified products were cloned into pYEura3 under the control of, and 3' to, the GAL1 promoter. The resulting plasmids were transformed into yeast as described in Example 1.

Yeast cultures containing full-length EL1 in λ YES and full-length EL2 in pYEura3 were grown in the presence of galactose or glucose as described in Example 2. Microsomes were then prepared from each of the cultures and fatty acid elongation assays were carried out as described in Example 2.

In the first experiment, microsomes were prepared from galactose-induced cultures of EL1, EL2 and FAE1, and incubated with either [1-¹⁴C] 18:0 acyl-CoA or [1-¹⁴C] 18:1 acyl-CoA as substrate. The amounts of various reaction products synthesized after 30 minutes (min) were determined as described in Example 2. The results when 18:0 acyl-CoA was the substrate are shown in Table 3. The results when 18:1 acyl-CoA was the substrate are shown in Table 4.

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Table 3.
Elongation of 18:0-CoA by FAE1, EL1 and EL2 Genes
Expressed in Yeast

Acyl-CoA Product	β -Keto Acyl Synthase Gene					
	FAE1		EL1		EL2	
	Rate ¹	(%)	Rate	(%)	Rate	(%)
20:0	0.369	64.3	0.084	89.8	0.108	41.8
22:0	0.113	18.6	0.047	21.9	0.053	20.7
24:0	0.065	10.7	0.043	19.9	0.052	20.3
26:0	0.038	6.3	0.042	19.4	0.044	17.2
Total	0.585	100.0	0.216	100.0	0.258	100.0

¹ Nanomoles/minute/mg of microsomal protein

Table 4.
Elongation of 18:1-CoA by FAE1, EL1 and EL2 Genes
Expressed in Yeast

Acyl-CoA Product	β -Keto Acyl Synthase Gene					
	FAE1		EL1		EL2	
	Rate ¹	(%)	Rate	(%)	Rate	(%)
20:1	1.131	84.6	0.111	80.8	0.091	84.1
22:1	0.206	15.4	0.026	19.2	0.017	15.9
24:1	0.0	0.0	0.0	0.0	0.0	0.0
26:1	0.0	0.0	0.0	0.0	0.0	0.0
Total	1.337	100.0	0.137	100.0	0.108	100.0

¹ Nanomoles/minute/mg of microsomal protein

The results shown in Tables 3 and 4 indicate that the EL1 and EL2 gene products have β -ketoacyl synthase (KAS) activity and that the KAS reaction product can be utilized to form VLCFAs. The specific activities of the 3 KAS enzymes cannot be compared, since the relative amount of the heterologous KAS protein in each microsomal preparation is not known. However, the proportions of various reaction products can be compared between FAE1, EL1 and EL2.

The data shown in Table 3 indicate that the EL1 and EL2 KAS activities result in a higher proportion of saturated VLCFAs than does the FAE1 KAS activity. These

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results suggest that EL1 and EL2 encode novel gene products, because EL1 and EL2 have a greater preference for C22:0 and C24:0 acyl-CoA substrates than does *FAE1*.

A comparison of the relative elongation activity of *FAE1* with 18:0 and 18:1 substrates (Tables 3 and 4) indicates that *FAE1* is more active when 18:1 is the substrate than when 18:0 is the substrate. In contrast, the overall rate of product formation with EL1 is less when 18:1 is the substrate than when 18:0 is the substrate (Tables 3 and 4). EL2 is also less active when 18:1 is the substrate than when 18:0 is the substrate (Tables 3 and 4). These results support the conclusion that EL1 and EL2 encode novel gene products and suggest that EL1 and EL2 have a preference for saturated fatty acids as substrates, whereas the *FAE1* gene product has a preference for monounsaturated fatty acids as substrates.

In a second experiment, microsomes were prepared from galactose-induced and from glucose-repressed yeast cultures containing EL1 or EL2 coding sequences. The microsomal preparations were incubated with either 18:0 acyl-CoA or 18:1 acyl-CoA as substrate and the fatty acid reaction products determined as described above. The results with the 18:0 substrate are shown in Table 5. The results with the 18:1 substrate are shown in Table 6.

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Table 5.
Elongation of 18:0-CoA by EL1 and EL2
With and Without Induction of Gene Expression

Acyl CoA	β -Keto Acyl Synthase Gene							
	EL1				EL2			
	+Glucose		+Galactose		+Glucose		+Galactose	
	Rate ¹	(%)	Rate	(%)	Rate	(%)	Rate	(%)
20:0	0.007	100.0	0.074	55.8	0.030	81.3	0.107	43.1
22:0	0.000	0.0	0.023	17.4	0.002	5.1	0.044	17.8
24:0	0.000	0.0	0.020	15.3	0.005	13.6	0.048	19.1
26:0	0.000	0.0	0.015	11.5	0.000	0.0	0.050	20.0
Total	0.007	100.0	0.133	100.0	0.037	100.0	0.249	100.0

¹ Nanomoles/minute/mg of microsomal protein

Table 6.
Elongation of 18:1-CoA by EL1 and EL2
With and Without Induction of Gene Expression

Acyl CoA	β -Keto Acyl Synthase Gene							
	EL1				EL2			
	+Glucose		+Galactose		+Glucose		+Galactose	
	Rate ¹	(%)	Rate	(%)	Rate	(%)	Rate	(%)
20:1	0.062	100.0	0.081	100.0	0.043	100.0	0.089	100.0
22:1	0.000	0.0	0.000	0.0	0.000	0.0	0.000	0.0
24:1	0.000	0.0	0.000	0.0	0.000	0.0	0.000	0.0
26:1	0.000	0.0	0.000	0.0	0.000	0.0	0.000	0.0
Total	0.062	100.0	0.081	100.0	0.043	100.0	0.089	100.0

¹ Nanomoles/minute/mg of microsomal protein

The results in Table 5 show *in vitro* elongase activity for EL1 and EL2 under induced (galactose) and uninduced (glucose) conditions. The comparison indicates that induction with galactose results in a large increase in overall elongase activity when 18:0 acyl CoA is the substrate (about 19-fold and 7-fold for EL1 and EL2, respectively). In contrast, induction when 18:1 acyl CoA is the substrate results in only a small increase in elongase activity (about 1.3-fold and 2-fold for EL1 and EL2, respectively), as shown in Table 6.

The results in Table 5 show that little or no VLCFA products are made by yeast microsomes under uninduced conditions. Upon induction of EL1 and EL2 gene

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expression, however, significant quantities of C20:0, C22:0, C24:0 and C26:0 are made. The data in Tables 5 and 6 are consistent with the results in Tables 3 and 4, which indicated that EL1 and EL2 were more active with a saturated fatty acid substrate than with a monounsaturated substrate.

The data in Tables 5 and 6 are also consistent with the data in Tables 3 and 4 indicating that the EL1 and EL2 gene products are more active in converting C24:0 to C26:0 than is *FAE1*.

In a third experiment, microsomes from induced and uninduced cultures containing EL1 or EL2 were incubated in the absence of cofactors involved in the β -ketoacyl condensation reaction. Cultures were induced and microsomes were prepared as described in Example 2. *In vitro* assays were carried out as described in Example 2, except that either ATP, CoASH or both were omitted from the enzyme reaction mixture. In addition, one reaction was carried out in a complete mixture having 0.01 mM of cerulenin (Sigma, St. Louis, MO). Cerulenin is an inhibitor of some condensing enzymes. The results are shown in Tables 7-9.

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Table 7.
Effect of Cofactors on 18:0-CoA Elongation¹

Gene	Expt ⁴	+Glu ²	+Gal ²	-ATP ³	-CoA ³	-A&C ³	+ Cer ³
EL1	1	.037	.109	.095	.105	.119	.141
	2	N.D.	.090	.125	.093	.270	.176
EL2	1	.033	.112	.168	.127	.143	.238
	2	N.D.	.120	.178	.133	.195	.302

¹ Activity in nanomoles/minute/mg of microsomal protein.

² +Glu: microsomes from cultures grown in the presence of glucose and incubated in standard reaction mix; +Gal: microsomes from cultures grown in the presence of galactose and incubated in standard reaction mix.

³ Microsomes from galactose-induced cultures. -ATP: ATP omitted from reaction mix; -CoA: Coenzyme A omitted from reaction mix; -A&C: ATP and Coenzyme A omitted from reaction mix; +Cer: Standard reaction mix containing 0.01 mM cerulenin.

⁴ Experiment No.

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Table 8.

Effect of Cofactors on Elongation Products of EL1¹

Prod.	+Glu ²	+Gal ²	-ATP ³	-CoA ³	-A&C ³	+Cer ³
20:0	53.9	46.2	34.4	47.8	41.7	46.7
22:0	14.4	18.7	13.7	18.0	19.4	16.2
24:0	18.5	18.1	20.6	19.1	16.7	17.7
26:0	13.2	17.1	31.4	15.2	22.3	19.4
Total	100.0	100.0	100.0	100.0	100.0	100.0

¹ Amount of indicated product as a percent of total products formed. Results of one experiment for +Glucose; Average of two experiments for other conditions.

² +Glu: microsomes from cultures grown in the presence of glucose and incubated in standard reaction mix; +Gal: microsomes from cultures grown in the presence of galactose and incubated in standard reaction mix.

³ Microsomes from galactose-induced cultures. -ATP: ATP omitted from reaction mix; -CoA: Coenzyme A omitted from reaction mix; -A&C: ATP and Coenzyme A omitted from reaction mix; +Cer: Standard reaction mix containing 0.01 mM cerulenin.

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Table 9.
Effect of Cofactors on Elongation Products of EL2¹

Prod.	+Glu ²	+Gal ²	-ATP ³	-CoA ³	-A&C ³	+Cer ³
20:0	54.5	47.1	34.1	45.3	38.0	41.8
22:0	17.1	19.1	16.4	19.2	15.9	16.1
24:0	5.8	19.4	20.8	19.9	18.4	20.4
26:0	22.6	14.5	28.9	15.8	27.8	21.8
Total	100.0	100.0	100.0	100.0	100.0	100.0

¹ Amount of indicated product as a percent of total products formed. Results of one experiment for +Glucose; Average of two experiments for other conditions.

² +Glu: microsomes from cultures grown in the presence of glucose and incubated in standard reaction mix; +Gal: microsomes from cultures grown in the presence of galactose and incubated in standard reaction mix.

³ Microsomes from galactose-induced cultures. -ATP: ATP omitted from reaction mix; -CoA: Coenzyme A omitted from reaction mix; -A&C: ATP and Coenzyme A omitted from reaction mix; +Cer: Standard reaction mix containing 0.01 mM cerulenin.

The results in Table 7 indicate that omission of ATP and/or CoA from the incubation mixture does not have a significant effect on the overall amounts of VLCFAs synthesized by the *in vitro* KAS activity of EL1 or EL2. The results also show that cerulenin does not inhibit the KAS activity of EL1 or EL2. The data in Table 8 and 9 confirm that EL1 and EL2 KAS activity produces significant amounts of C24:0 and C26:0 acyl CoA products.

To the extent not already indicated, it will be understood by those of ordinary skill in the art that any one of the various specific embodiments herein described and illustrated may be further modified to incorporate features shown in other of the specific embodiments.

The foregoing detailed description has been provided for a better understanding of the invention only and no unnecessary limitation should be understood therefrom as some modifications will be apparent to those

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skilled in the art without deviating from the spirit and scope of the appended claims.

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SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: CARGILL, INCORPORATED
- (ii) TITLE OF THE INVENTION: FATTY ACID ELONGASES
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C., P.A.
 - (B) STREET: 60 South Sixth Street, Suite 3300
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/868,373
 - (B) FILING DATE: 03-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lundquist, Ronald C
 - (B) REGISTRATION NUMBER: 37,875
 - (C) REFERENCE/DOCKET NUMBER: 07039/064W01
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-335-5050
 - (B) TELEFAX: 612-288-9696
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGATCGAG	AGAGATTAAC	GCGGAGATG	GCGTTTCGAG	ATTCATCATC	GGCCGTTATA	60
AGAATTCGAA	GACGTTTGCC	GGATTTATTA	ACGTCCGTTA	AGCTCAAATA	CGTGAAGCTT	120
GGACTTCACA	ACTCTTGCAA	CGTGACCACC	ATTCTCTTCT	TCTTAATTAT	TCTTCCTTTA	180
ACCGGAACCG	TGCTGGTTCA	GCTAACCGGT	CTAACGTTTCG	ATACGTTCTC	TGAGCTTTGG	240
TCTAACCAGG	CGGTTCAACT	CGACACGGCG	ACGAGACTTA	CCTGCTTGGT	TTTCCTCTCC	300
TTCGTTTGA	CCCTCTACGT	GGCTAACCGG	TCTAAACCGG	TTTACCTAGT	GGATTTCTCC	360
TGCTACAAAC	CGGAAGACGA	GCGTAAATA	TCAGTAGATT	CGTTCCTTGAC	GATGACTGAG	420
GAAATGGAT	CATTCACCGA	TGACACGGTT	CAGTTCCAGC	AAAGAATCTC	GAACCGGGCC	480

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GGTTTGGGAG ACGAGACGTA TCTGCCACGT GGCATAACTT CAACGCCCCC GAAGCTAAAT 540
ATGTCAGAGG CACGTGCCGA AGCTGAAGCC GTTATGTTTG GAGCCTTAGA TTCCCTCTTC 600
GAGAAAACCG GAATTAAACC GGCCGAAGTC GGAATCTTGA TAGTAAACTG CAGCTTATTC 660
AATCCGACGC CGTCTCTATC AGCGATGATC GTGAACCATT ACAAGATGAG AGAAGACATC 720
AAAAGTTACA ACCTCGGAGG AATGGGTTGC TCCGCCGGAT TAATCTCAAT CGATCTCGCT 780
AACAATCTCC TCAAAGCAAA CCCTAATTCT TACGCTGTCTG TGGTAAGCAC GGAAAACATA 840
ACCCTAAACT GGTACTTCGG AAATGACCGG TCAATGCTCC TCTGCAACTG CATCTTCCGA 900
ATGGGCGGAG CTGCGATTCT CCTCTCTAAC CGCCGTCAAG ACCGGAAGAA GTCAAAGTAC 960
TCGCTGGTCA ACGTCGTTTC AACACATAAA GGATCAGACG ACAAGAACTA CAATTGCGTG 1020
TACCAGAAGG AAGACGAGAG AGGAACAATC GGTGTCTCTT TAGCTAGAGA GCTCATGTCT 1080
GTCGCCGGAG ACGCTCTGAA AACAAACATC ACGACTTTAG GACCGATGGT TCTTCCATTG 1140
TCAGAGCAGT TGATGTTCTT GATTTCTTTG GTCAAAAGGA AGATGTTCAA GTTAAAAGTT 1200
AAACCGTATA TTCCGGATTT CAAGCTAGCT TTCGAGCATT TCTGTATTCA CGCAGGAGGT 1260
AGAGCGGTTT TAGACGAAGT GCAGAAGAAT CTTGATCTCA AAGATTGGCA CATGGAACCT 1320
TCTAGAATGA CTTTGCACAG ATTTGGTAAC ACTTCGAGTA GCTCGCTTTG GTATGAGATG 1380
GCTTATACCG AAGCTAAGGG TCGGGTTAAA GCTGGTGACC GACTTTGGCA GATTGCGTTT 1440
GGATCGGGTT TCAAGTGTA TAGTGCGGTT TGGAAAGCGT TACGACCGGT TTCGACGGAG 1500
GAGATGACCG GTAATGCTTG GGCTGGTTTC ATTGATCAAT ATCCGGTTAA AGTTGTGCAA 1560

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Asp Arg Glu Arg Leu Thr Ala Glu Met Ala Phe Arg Asp Ser Ser
 1           5           10           15
Ser Ala Val Ile Arg Ile Arg Arg Arg Leu Pro Asp Leu Leu Thr Ser
          20          25          30
Val Lys Leu Lys Tyr Val Lys Leu Gly Leu His Asn Ser Cys Asn Val
          35          40          45
Thr Thr Ile Leu Phe Phe Leu Ile Ile Leu Pro Leu Thr Gly Thr Val
          50          55          60
Leu Val Gln Leu Thr Gly Leu Thr Phe Asp Thr Phe Ser Glu Leu Trp
65          70          75          80
Ser Asn Gln Ala Val Gln Leu Asp Thr Ala Thr Arg Leu Thr Cys Leu
          85          90          95
Val Phe Leu Ser Phe Val Leu Thr Leu Tyr Val Ala Asn Arg Ser Lys
          100         105         110
Pro Val Tyr Leu Val Asp Phe Ser Cys Tyr Lys Pro Glu Asp Glu Arg
          115         120         125
Lys Ile Ser Val Asp Ser Phe Leu Thr Met Thr Glu Glu Asn Gly Ser
130         135         140
Phe Thr Asp Asp Thr Val Gln Phe Gln Gln Arg Ile Ser Asn Arg Ala
145         150         155         160
Gly Leu Gly Asp Glu Thr Tyr Leu Pro Arg Gly Ile Thr Ser Thr Pro
          165         170         175
Pro Lys Leu Asn Met Ser Glu Ala Arg Ala Glu Ala Glu Ala Val Met
          180         185         190
Phe Gly Ala Leu Asp Ser Leu Phe Glu Lys Thr Gly Ile Lys Pro Ala
          195         200         205
Glu Val Gly Ile Leu Ile Val Asn Cys Ser Leu Phe Asn Pro Thr Pro
          210         215         220
Ser Leu Ser Ala Met Ile Val Asn His Tyr Lys Met Arg Glu Asp Ile
225         230         235         240
Lys Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser
          245         250         255
Ile Asp Leu Ala Asn Asn Leu Leu Lys Ala Asn Pro Asn Ser Tyr Ala
          260         265         270
Val Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Phe Gly Asn
          275         280         285

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Asp	Arg	Ser	Met	Leu	Leu	Cys	Asn	Cys	Ile	Phe	Arg	Met	Gly	Gly	Ala	
290						295					300					
Ala	Ile	Leu	Leu	Ser	Asn	Arg	Arg	Gln	Asp	Arg	Lys	Lys	Ser	Lys	Tyr	
305					310					315					320	
Ser	Leu	Val	Asn	Val	Arg	Thr	His	Lys	Gly	Ser	Asp	Asp	Lys	Asn		
			325					330					335			
Tyr	Asn	Cys	Val	Tyr	Gln	Lys	Glu	Asp	Glu	Arg	Gly	Thr	Ile	Gly	Val	
			340					345					350			
Ser	Leu	Ala	Arg	Glu	Leu	Met	Ser	Val	Ala	Gly	Asp	Ala	Leu	Lys	Thr	
		355					360					365				
Asn	Ile	Thr	Thr	Leu	Gly	Pro	Met	Val	Leu	Pro	Leu	Ser	Glu	Gln	Leu	
						375					380					
Met	Phe	Leu	Ile	Ser	Leu	Val	Lys	Arg	Lys	Met	Phe	Lys	Leu	Lys	Val	
385					390					395					400	
Lys	Pro	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Glu	His	Phe	Cys	Ile	
			405						410					415		
His	Ala	Gly	Gly	Arg	Ala	Val	Leu	Asp	Glu	Val	Gln	Lys	Asn	Leu	Asp	
			420					425					430			
Leu	Lys	Asp	Trp	His	Met	Glu	Pro	Ser	Arg	Met	Thr	Leu	His	Arg	Phe	
		435					440					445				
Gly	Asn	Thr	Ser	Ser	Ser	Ser	Leu	Trp	Tyr	Glu	Met	Ala	Tyr	Thr	Glu	
		450				455					460					
Ala	Lys	Gly	Arg	Val	Lys	Ala	Gly	Asp	Arg	Leu	Trp	Gln	Ile	Ala	Phe	
465					470					475					480	
Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	Trp	Lys	Ala	Leu	Arg	Pro	
			485						490					495		
Val	Ser	Thr	Glu	Glu	Met	Thr	Gly	Asn	Ala	Trp	Ala	Gly	Ser	Ile	Asp	
			500					505					510			
Gln	Tyr	Pro	Val	Lys	Val	Val	Gln									
		515					520									

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGATTACC	CCATGAAGAA	GGTAAAAATC	TTTTTCAACT	ACCTCATGGC	GCATCGCTTC	60
AAGCTCTGCT	TCCTTACCATT	AATGGTTGCT	ATAGCCGTGG	AGGCGTCTCG	TC'TTTCACA	120
CAAGATCTCC	AAAAC'TTTTA	CCTCTACTTA	CAAAACAACC	ACACATCTCT	AACCATGTTC	180
TTCCTTTACC	TCGCTCTCGG	GTCGACTCTT	TACCTCATGA	CCCGGCCCAA	ACCCGTTTAT	240
CTCGTTGACT	TTAGCTGCTA	CCTCCCACCG	TCGCATCTCA	AAGCCAGCAC	CCAGAGGATC	300
ATGCAACACG	TAAGGCTTGT	ACGAGAAGCA	GGCGCGTGGA	AGCAAGAGTC	CGATTACTTG	360
ATGGACTTCT	GCGAGAAGAT	TCTAGAACGT	TCCGGTCTAG	GCCAAGAGAC	GTACGTACCC	420
GAAGGTCTTC	AAACTTTGCC	ACTACAACAG	AATTTGGCTG	TATCACGTAT	AGAGACGGAG	480
GAAGTTATTA	TTGGTGCGGT	CGATAATCTG	TTTCGCAACA	CGGGAATAAG	CCCTAGTGAT	540
ATAGGTATAT	TGGTGGTGAA	TTCAAGCACT	TTTAATCCAA	CACCTTCGCT	ATCAAGTATC	600
TTAGTGAATA	AGTTTAAACT	TAGGGATAAT	ATAAAGAGCT	TGAATCTTGG	TGGGATGGGG	660
TGTAGCGCTG	GAGTCATCGC	TATCGATGCG	GCTAAGAGCT	TGTTACAAGT	TCATAGAAAC	720
ACTTATGCTC	TTGTGGTGAG	CACGGAGAAC	ATCACTCAAA	ACTTGTTACAT	GGGTAACAAC	780
AAATCAATGT	TGGTTACAAA	CTGTTTGTTC	CGTATAGGTG	GGGCCGCGAT	TTTGCTTTCT	840
AACCGGTCTA	TAGATCGTAA	ACGCGCAAAA	TACGAGCTTG	TTCACACCGT	GCGGGTCCAT	900
ACCGGAGCAG	ATGACCGATC	CTATGAATGT	GCAACTCAAG	AAGAGGATGA	AGATGGCATA	960
GTTGGGGTTT	CC'TTGTCAA	GAATCTACCA	ATGGTAGCTG	CAAGAACCCT	AAAGATCAAT	1020
ATCGCAACTT	TGGGTCCGCT	TGTTCTTCCC	ATAAGCGAGA	AGTTTCACTT	CTTTGTGAGG	1080
TTCTGTTAAAA	AGAAGTTTCT	CAACCCCAAG	CTAAAGCATT	ACATTCCGGA	TTTCAAGCTC	1140
GCATTCGAGC	ATTTCTGTAT	CCATGCGGGT	GGTAGAGCGC	TAATTGATGA	GATGGAGAAG	1200
AATCTTCATC	TAAC'TCCACT	AGACGTTGAG	GCTTCAAGAA	TGACATTACA	CAGGTTTGGT	1260
AATACCTCTT	CGAGCTCCAT	TTGGTACGAG	TTGGCTTACA	CAGAAGCCAA	AGGAAGGATG	1320
ACGAAAGGAG	ATAGGATTTG	GCAGATTGCG	TTGGGGTCAG	GTTTTAAGTG	TAATAGTTCA	1380

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GTTTGGGTGG CTCTTCGTAA CGTCAAGCCT TCTACTAATA ATCCTTGGGA ACAGTGTCTA 1440
 CACAAATATC CAGTTGAGAT CGATATAGAT TTAAAAGAG 1479

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Tyr	Pro	Met	Lys	Lys	Val	Lys	Ile	Phe	Phe	Asn	Tyr	Leu	Met
1				5					10					15	
Ala	His	Arg	Phe	Lys	Leu	Cys	Phe	Leu	Pro	Leu	Met	Val	Ala	Ile	Ala
			20					25					30		
Val	Glu	Ala	Ser	Arg	Leu	Ser	Thr	Gln	Asp	Leu	Gln	Asn	Phe	Tyr	Leu
			35				40					45			
Tyr	Leu	Gln	Asn	Asn	His	Thr	Ser	Leu	Thr	Met	Phe	Phe	Leu	Tyr	Leu
	50				55					60					
Ala	Leu	Gly	Ser	Thr	Leu	Tyr	Leu	Met	Thr	Arg	Pro	Lys	Pro	Val	Tyr
65				70					75					80	
Leu	Val	Asp	Phe	Ser	Cys	Tyr	Leu	Pro	Pro	Ser	His	Leu	Lys	Ala	Ser
			85					90					95		
Thr	Gln	Arg	Ile	Met	Gln	His	Val	Arg	Leu	Val	Arg	Glu	Ala	Gly	Ala
			100					105					110		
Trp	Lys	Gln	Glu	Ser	Asp	Tyr	Leu	Met	Asp	Phe	Cys	Glu	Lys	Ile	Leu
	115				120							125			
Glu	Arg	Ser	Gly	Leu	Gly	Gln	Glu	Thr	Tyr	Val	Pro	Glu	Gly	Leu	Gln
	130				135					140					
Thr	Leu	Pro	Leu	Gln	Gln	Asn	Leu	Ala	Val	Ser	Arg	Ile	Glu	Thr	Glu
145				150					155					160	
Glu	Val	Ile	Ile	Gly	Ala	Val	Asp	Asn	Leu	Phe	Arg	Asn	Thr	Gly	Ile
			165					170					175		
Ser	Pro	Ser	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Thr	Phe	Asn
			180				185						190		
Pro	Thr	Pro	Ser	Leu	Ser	Ser	Ile	Leu	Val	Asn	Lys	Phe	Lys	Leu	Arg
	195						200					205			
Asp	Asn	Ile	Lys	Ser	Leu	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly
	210				215					220					
Val	Ile	Ala	Ile	Asp	Ala	Ala	Lys	Ser	Leu	Leu	Gln	Val	His	Arg	Asn
225				230					235					240	
Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Asn	Leu	Tyr
			245					250					255		
Met	Gly	Asn	Asn	Lys	Ser	Met	Leu	Val	Thr	Asn	Cys	Leu	Phe	Arg	Ile
			260				265					270			
Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Arg	Ser	Ile	Asp	Arg	Lys	Arg
	275						280					285			
Ala	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Val	His	Thr	Gly	Ala	Asp
	290					295					300				
Asp	Arg	Ser	Tyr	Glu	Cys	Ala	Thr	Gln	Glu	Glu	Asp	Glu	Asp	Gly	Ile
305				310					315					320	
Val	Gly	Val	Ser	Leu	Ser	Lys	Asn	Leu	Pro	Met	Val	Ala	Ala	Arg	Thr
			325					330					335		
Leu	Lys	Ile	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	Ile	Ser
			340				345					350			
Glu	Lys	Phe	His	Phe	Phe	Val	Arg	Phe	Val	Lys	Lys	Lys	Phe	Leu	Asn
	355					360					365				
Pro	Lys	Leu	Lys	His	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Glu	His
	370				375						380				
Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Leu	Ile	Asp	Glu	Met	Glu	Lys
385				390					395					400	
Asn	Leu	His	Leu	Thr	Pro	Leu	Asp	Val	Glu	Ala	Ser	Arg	Met	Thr	Leu
			405					410						415	

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His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala
 420 425 430
 Tyr Thr Glu Ala Lys Gly Arg Met Thr Lys Gly Asp Arg Ile Trp Gln
 435 440 445
 Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ser Val Trp Val Ala
 450 455 460
 Leu Arg Asn Val Lys Pro Ser Thr Asn Asn Pro Trp Glu Gln Cys Leu
 465 470 475 480
 His Lys Tyr Pro Val Glu Ile Asp Ile Asp Leu Lys Glu
 485 490

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTACGTCAGG	GTAGAACAAA	GAGTAAACAC	TTAAGCAAAA	CAATTGTGCC	TACTCTTAGG	60
TTATCTCCAA	TGAAGAACTT	AAAGATGGTT	TTCTTCAAGA	TCCTCTTTAT	CTCTTTAATG	120
GCAGGATTAG	CCATGAAAGG	ATCTAAGATC	AACGTAGAAG	ATCTCCAAAA	GTTCTCCCTC	180
CACCATACAC	AGAACAACCT	CCAAACCATA	AGCCTTCTAT	TGTTTCTTGT	CGTTTTTGTG	240
TGGATCCTCT	ACATGTTAAC	CCGACCTAAA	CCCGTTTACC	TTGTTGATTT	CTCCTGCTAC	300
CTTCCACCGT	CGCATCTCAA	GGTCAGTATC	CAAACCCTAA	TGGGACACGC	AAGACGTGCA	360
AGAGAAGCAG	GCATGTGTTG	GAAGAACAAA	GAGAGCGACC	ATTTAGTTGA	CTTCCAGGAG	420
AAGATTCTTG	AACGTTCCGG	TCTTGGTCAA	GAAACCTACA	TCCCGAGGGG	TCTTCAGTGC	480
TTCCCACTTC	AGCAAGGCAT	GGGTGCTTCA	CGTAAAGAGA	CGGAAGAAGT	AATCTTCGGA	540
GCTCTTGACA	ATCTTTTTTCG	CAACACCGGT	GTAAACCTTG	ATGATATCGG	TATATTGGTG	600
GTGAATTCTA	GCACGTTTAA	TCCAACCTCA	TCACTCGCCT	CCATGATTGT	GAACAAGTAC	660
AAACTCAGAG	ACAACATCAA	GAGTTTGAAT	CTTGGAGGGA	TGGGTTGCAG	TGCCGGAGTT	720
ATAGCTGTTG	ATGTCGCTAA	GGGATTACTA	CAAGTTCATA	GGAACACTTA	TGCTATTGTA	780
GTAAGCACAG	AGAACATCAC	TCAGAACTTA	TACTTGGGGA	AAAACAAATC	AATGCTAGTC	840
ACAAACTGTT	TGTTCCGCGT	TGGTGGTGCT	GCGGTTCTGC	TTTCAAACAG	ATCTAGAGAC	900
CGTAACCGCG	CCAAATACGA	GCTTGTTTCA	ACCGTACGGA	TCCATACCGG	ATCAGATGAT	960
AGGTCGTTTC	AATGTGCGAC	ACAAGAAGAG	GATGAAGATG	GTATAATTGG	AGTTACCTTG	1020
ACAAAGAATC	TACCTATGGT	GGCTGCAAGG	ACTCTTAAGA	TAAATATCGC	AACCTTTGGGT	1080
CCTCTTGATC	TTCCATTAAA	AGAGAAGCTA	GCCTTCTTTA	TTACTTTTGT	CAAGAAGAAG	1140
TATTTCAAGC	CAGAGTTAAG	GAATTATACA	CCAGATTTCA	AGCTTGCCTT	TGAGCATTTT	1200
TGTATCCACG	CTGGTGGAAG	AGCTCTAATA	GATGAGCTGG	AGAAGAACCT	TAAGCTTTCT	1260
CCGTTACACG	TAGAGGCGTC	AAGAATGACA	CTACACAGGT	TTGGTAACAC	TTCTTCTAGC	1320
TCAATCTGGT	ACGAGTTAGC	TTATACAGAA	GCTAAAGGAA	GGATGAAGGA	AGGAGATAGG	1380
ATTTGGCAGA	TTGCTTTGGG	GTCAGGTTTT	AAGTGTAACA	GTTTCAGTATG	GGTGGCTCTG	1440
CGAGACGTTA	AGCCTTCAGC	TAACAGTCCA	TGGGAAGACT	GTATGGATAG	ATATCCGGTT	1500
GAGATTGATA	TT					1512

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Arg Gln Gly Arg Thr Lys Ser Lys His Leu Ser Lys Thr Ile Cys
 1 5 10 15
 Pro Thr Leu Arg Leu Ser Pro Met Lys Asn Leu Lys Met Val Phe Phe
 20 25 30

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1650 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGGGTAGAT	CCAACGAGCA	AGATCTGCTC	TCTACCGAGA	TCGTTAATCG	TGGGATCGAA	60
CCATCCGGTC	CTAACGCCGG	CTCACCAACG	TTCTCGGTTA	GGGTCAGGAG	ACGTTTGCCCT	120
GATTTTCTTC	AGTCGGTGAA	CTTGAAGTAC	GTGAAACTTG	GTTACCACTA	CCTCATAAAC	180
CATGCGGTTT	ATTTGGCGAC	CATACCGGTT	CTTGTGCTGG	TTTTTAGTGC	TGAGGTTGGG	240
AGTTTAAGCA	GAGAAGAGAT	TTGGAAGAAG	CTTTGGGACT	ATGATCTTGC	AACTGTTATC	300
GGATTCTTCG	GTGCTTTTGT	TTTAACCGCT	TGTGCTACT	TCATGTCCTG	TCCTCGCTCT	360
GTTTATCTTA	TTGATTTTCG	TTGTTACAAG	CCCTCCGATG	AACACAAGGT	GACAAAAGAA	420
GAGTTCATAG	AACTAGCGAG	AAAATCAGGG	AAGTTCGACG	AAGAGACACT	CGGTTTCAAG	480
AAGAGGATCT	TACAAGCCTC	AGGCATAGGC	GACGAGACAT	ACGTCCCAAG	ATCCATCTCT	540
TCATCAGAAA	ACATAACAAC	GATGAAAGAA	GGTCGTGAAG	AAGCCTCTAC	AGTGATCTTT	600
GGAGCACTAG	ACGAACTCTT	CGAGAAGACA	CGTGTAAGAC	CTAAAGACGT	TGGTGTCCCT	660
GTGGTTAACT	GTAGCATTTT	CAACCCGACA	CCGTCGTTGT	CCGCAATGGT	GATAAACCAT	720
TACAAGATGA	GAGGGAACAT	ACTTAGTTAC	AACCTTGGAG	GGATGGGATG	TTTCGGCTGGA	780
ATCATAGCTA	TTGATCTTGC	TCGTGACATG	CTTCAGTCTA	ACCCTAATAG	TTATGCTGTT	840
GTTGTGAGTA	CTGAGATGGT	TGGGTATAAT	TGGTACGTGG	GAAGTGACAA	GTCAATGGTT	900
ATACCTAATT	GTTTCTTTAG	GATGGGTTGT	TCTGCCGTTA	TGCTCTCTAA	CCGTCGTCGT	960
GACTTTCGCC	ATGCTAAGTA	CCGTCTCGAG	CACATTGTCC	GAAGTGAAC	AAGGATTCAA	1020
GACCGTAGCT	TCAGGAGTGT	GTACCAGGAA	GAAGATGAAC	AAGGATTCAA	GGGGTTGAAG	1080
ATAAGTAGAG	ACTTAATGGA	AGTTGGAGGT	GAAGCTCTCA	AGACAAACAT	CACTACCTTA	1140
GGTCCTCTTG	TCCTACCTTT	CTCCGAGCAG	CTTCTCTTCT	TTGCTGCTTT	GGTCCGCCGA	1200
ACATTCTCAC	CTGCTGCCAA	AACGTCCACA	ACCACTTCCT	TCTCTACTTC	CGCCACCGCA	1260
AAAACCAATG	GAATCAAGTC	TTCCTCTTCC	GATCTGTCCA	AGCCATACAT	CCCGGACTAC	1320
AAGCTCGCCT	TCGAGCATTT	TTGCTTCCAC	GCGGCAAGCA	AAGTAGTGCT	TGAAGAGCTT	1380
CAAAAGAATC	TAGGCTTGAG	TGAAGAGAAT	ATGGAGGCTT	CTAGGATGAC	ACTTCACAGG	1440
TTTGGAACAA	CTTCTAGCAG	TGGAATCTGG	TATGAGTTGG	CTTACATGGA	GGCCAAGGAA	1500
AGTGTTCGTA	GAGGCGATAG	GGTTTGGCAG	ATCGCTTTTCG	GTTCTGGTTT	TAAGTGTAAAC	1560
AGTGTGGTGT	GGAAGGCAAT	GAGGAAGGTG	AAGAAGCCAA	CCAGGAACAA	TCCTTGGGGTG	1620
GATTGCATCA	ACCGTTACCC	TGTGCCTCTC				1650

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gly	Arg	Ser	Asn	Glu	Gln	Asp	Leu	Leu	Ser	Thr	Glu	Ile	Val	Asn
1				5				10						15	
Arg	Gly	Ile	Glu	Pro	Ser	Gly	Pro	Asn	Ala	Gly	Ser	Pro	Thr	Phe	Ser
			20					25					30		
Val	Arg	Val	Arg	Arg	Arg	Leu	Pro	Asp	Phe	Leu	Gln	Ser	Val	Asn	Leu
			35				40					45			
Lys	Tyr	Val	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	Asn	His	Ala	Val	Tyr
			50			55					60				
Leu	Ala	Thr	Ile	Pro	Val	Leu	Val	Leu	Val	Phe	Ser	Ala	Glu	Val	Gly
65					70					75				80	
Ser	Leu	Ser	Arg	Glu	Glu	Ile	Trp	Lys	Lys	Leu	Trp	Asp	Tyr	Asp	Leu
			85					90						95	
Ala	Thr	Val	Ile	Gly	Phe	Phe	Gly	Val	Phe	Val	Leu	Thr	Ala	Cys	Val
			100					105						110	

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Tyr	Phe	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Ile	Asp	Phe	Ala	Cys
		115					120					125			
Tyr	Lys	Pro	Ser	Asp	Glu	His	Lys	Val	Thr	Lys	Glu	Glu	Phe	Ile	Glu
	130					135					140				
Leu	Ala	Arg	Lys	Ser	Gly	Lys	Phe	Asp	Glu	Glu	Thr	Leu	Gly	Phe	Lys
145					150					155					160
Lys	Arg	Ile	Leu	Gln	Ala	Ser	Gly	Ile	Gly	Asp	Glu	Thr	Tyr	Val	Pro
			165						170					175	
Arg	Ser	Ile	Ser	Ser	Ser	Glu	Asn	Ile	Thr	Thr	Met	Lys	Glu	Gly	Arg
			180				185						190		
Glu	Glu	Ala	Ser	Thr	Val	Ile	Phe	Gly	Ala	Leu	Asp	Glu	Leu	Phe	Glu
	195						200					205			
Lys	Thr	Arg	Val	Lys	Pro	Lys	Asp	Val	Gly	Val	Leu	Val	Val	Asn	Cys
	210					215					220				
Ser	Ile	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Ile	Asn	His
225					230					235					240
Tyr	Lys	Met	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly
				245					250					255	
Cys	Ser	Ala	Gly	Ile	Ile	Ala	Ile	Asp	Leu	Ala	Arg	Asp	Met	Leu	Gln
			260					265					270		
Ser	Asn	Pro	Asn	Ser	Tyr	Ala	Val	Val	Val	Ser	Thr	Glu	Met	Val	Gly
		275					280					285			
Tyr	Asn	Trp	Tyr	Val	Gly	Ser	Asp	Lys	Ser	Met	Val	Ile	Pro	Asn	Cys
	290					295					300				
Phe	Phe	Arg	Met	Gly	Cys	Ser	Ala	Val	Met	Leu	Ser	Asn	Arg	Arg	Arg
305					310					315					320
Asp	Phe	Arg	His	Ala	Lys	Tyr	Arg	Leu	Glu	His	Ile	Val	Arg	Thr	His
			325						330					335	
Lys	Ala	Ala	Asp	Asp	Arg	Ser	Phe	Arg	Ser	Val	Tyr	Gln	Glu	Glu	Asp
			340					345					350		
Glu	Gln	Gly	Phe	Lys	Gly	Leu	Lys	Ile	Ser	Arg	Asp	Leu	Met	Glu	Val
	355					360						365			
Gly	Gly	Glu	Ala	Leu	Lys	Thr	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val
	370					375					380				
Leu	Pro	Phe	Ser	Glu	Gln	Leu	Leu	Phe	Phe	Ala	Ala	Leu	Val	Arg	Arg
385					390					395					400
Thr	Phe	Ser	Pro	Ala	Ala	Lys	Thr	Ser	Thr	Thr	Thr	Ser	Phe	Ser	Thr
				405					410					415	
Ser	Ala	Thr	Ala	Lys	Thr	Asn	Gly	Ile	Lys	Ser	Ser	Ser	Ser	Asp	Leu
			420				425						430		
Ser	Lys	Pro	Tyr	Ile	Pro	Asp	Tyr	Lys	Leu	Ala	Phe	Glu	His	Phe	Cys
		435					440					445			
Phe	His	Ala	Ala	Ser	Lys	Val	Val	Leu	Glu	Glu	Leu	Gln	Lys	Asn	Leu
	450					455					460				
Gly	Leu	Ser	Glu	Glu	Asn	Met	Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg
465					470					475					480
Phe	Gly	Asn	Thr	Ser	Ser	Ser	Gly	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Met
				485					490					495	
Glu	Ala	Lys	Glu	Ser	Val	Arg	Arg	Gly	Asp	Arg	Val	Trp	Gln	Ile	Ala
			500					505					510		
Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Val	Val	Trp	Lys	Ala	Met	Arg
		515					520					525			
Lys	Val	Lys	Lys	Pro	Thr	Arg	Asn	Asn	Pro	Trp	Val	Asp	Cys	Ile	Asn
	530					535					540				
Arg	Tyr	Pro	Val	Pro	Leu										
545					550										

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCGAGCTACG	TCAGGGCTTT	TATATGCACA	AATTCTCATA	AAGTTTTC	TTTATTCCA	60
TTTTTCTCGG	AAGCCATGGA	AGCTGCTAAT	GAGCCTGTTA	ATGGCGGATC	CGTACAGATC	120
CGAACAGAGA	ACAACGAAAG	ACGAAAGCTT	CCTAATTTCT	TACAAAGCGT	CAACATGAAA	180
TACGTCAAGC	TAGCTTATCA	TTACCTCATT	ACTCATCTCT	TCAAGCTCTG	TTTGGTTCCA	240
TTAATGGCGG	TTTTAGTCAC	AGAGATCTCT	CGATTAAACA	CAGACGATCT	TTACCAGATT	300
TGGCTTCATC	TCCAATACAA	TCTCGTTGCT	TTCATCTTTC	TCTCTGCTTT	AGCTATCTTT	360
GGCTCCACCG	TTTACATCAT	GAGTCGTCCC	AGATCTGTTT	ATCTCGTTGA	TTACTCTTGT	420
TATCTTCCTC	CGGAGAGTCT	TCAGGTAAAG	TATCAGAAAGT	TTATGGATCA	TTCTAAGTTG	480
ATTGAAGATT	TCAATGAGTC	ATCTTTAGAG	TTTCAGAGGA	AGATTCTTGA	ACGTTCTGGT	540
TTAGGAGAAG	AGACTTATCT	CCCTGAAGCT	TTACATTGTA	TCCCTCCGAG	GCCTACGATG	600
ATGGCGGCTC	GTGAGGAATC	TGAGCAGGTA	ATGTTTGGTG	CTCTTGATAA	GCTTTTCGAG	660
AATACCAAGA	TTAACCTTAG	GGATATTGGT	GTGTTGGTTG	TGAATTGTAG	CTTGTTTAAT	720
CCTACACCTT	CGTTGTCAGC	TATGATTGTT	AACAAGTATA	AGCTTAGAGG	GAATGTTAAG	780
AGTTTTAACC	TTGGTGGAAT	GGGGTGTAGT	GCTGGTGTTA	TCTCTATCGA	TTTAGCTAAA	840
GATATGTTGC	AAGTTCATAG	GAATACTTAT	GCTGTTGTGG	TTAGTACTGA	GAACATTACT	900
CAGAATTGGT	ATTTTGGGAA	TAAGAAGGCT	ATGTTGATTG	CGAATTGTTT	GTTTCGTGTT	960
GGTGGTTCGG	CGATTTTGTT	GTCGAACAAG	GGGAAAGATC	GTAGACGGTC	TAAGTATAAG	1020
CTTGTTTCATA	CCGTTAGGAC	TCATAAAGGA	GCTGTTGAGA	AGGCTTTC	CTGTGTTTAC	1080
CAAGAGCAAG	ATGATAATGG	GAAGACCGGG	GTTTCGTTGT	CGAAAGATCT	TATGGCTATA	1140
GCTGGGGAAG	CTCTTAAGGC	GAATATCACT	ACTTTAGGTC	CTTTGGTTCT	TCCTATAAGT	1200
GAGCAGATTC	TGTTTTTCAT	GACTTTGGTT	ACGAAGAAAC	TGTTTAACTC	GAAGCTGAAG	1260
CCGTATATTC	CGGATTTCAA	GCTTGCGTTT	GATCATTTCT	GTATCCATGC	TGGTGGTAGA	1320
GCTGTGATTG	ATGAGCTTGA	GAAGAATCTG	CAGCTTTCGC	AGACTCATGT	CGAGGACTCC	1380
AGAATGACAC	TGCACAGATT	TGGAAACACT	TCTTCGAGCT	CGATTTGCTA	TGAACTGGCT	1440
TACATAGAGG	CTAAAGGTAG	GATGAAGAAA	GGAAACCGGG	TTTGGCAGAT	TGCTTTTGGG	1500
AGTGGGTTTA	AGTGTAACAG	TGCAGTTTGG	GTGGCTCTAA	ACAATGTCAA	GCCTTCGGTT	1560
AGTAGTCCGT	GGGAACACTG	CATCGACCGA	TATCCGGTTA	AGCTCGACTT	C	1611

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser	Ser	Tyr	Val	Arg	Ala	Phe	Ile	Cys	Thr	Asn	Ser	His	Lys	Val	Phe
1				5					10					15	
Asn	Phe	Ile	Pro	Phe	Phe	Ser	Glu	Ala	Met	Glu	Ala	Ala	Asn	Glu	Pro
			20					25					30		
Val	Asn	Gly	Gly	Ser	Val	Gln	Ile	Arg	Thr	Glu	Asn	Asn	Glu	Arg	Arg
		35					40					45			
Lys	Leu	Pro	Asn	Phe	Leu	Gln	Ser	Val	Asn	Met	Lys	Tyr	Val	Lys	Leu
	50					55					60				
Gly	Tyr	His	Tyr	Leu	Ile	Thr	His	Leu	Phe	Lys	Leu	Cys	Leu	Val	Pro
65					70				75					80	
Leu	Met	Ala	Val	Leu	Val	Thr	Glu	Ile	Ser	Arg	Leu	Thr	Thr	Asp	Asp
			85					90						95	
Leu	Tyr	Gln	Ile	Trp	Leu	His	Leu	Gln	Tyr	Asn	Leu	Val	Ala	Phe	Ile
		100						105					110		
Phe	Leu	Ser	Ala	Leu	Ala	Ile	Phe	Gly	Ser	Thr	Val	Tyr	Ile	Met	Ser
		115					120					125			
Arg	Pro	Arg	Ser	Val	Tyr	Leu	Val	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro
	130					135					140				
Glu	Ser	Leu	Gln	Val	Lys	Tyr	Gln	Lys	Phe	Met	Asp	His	Ser	Lys	Leu
145					150					155				160	
Ile	Glu	Asp	Phe	Asn	Glu	Ser	Ser	Leu	Glu	Phe	Gln	Arg	Lys	Ile	Leu
			165						170					175	
Glu	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	Glu	Ala	Leu	His
			180					185						190	

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Cys	Ile	Pro	Pro	Arg	Pro	Thr	Met	Met	Ala	Ala	Arg	Glu	Glu	Ser	Glu
		195					200					205			
Gln	Val	Met	Phe	Gly	Ala	Leu	Asp	Lys	Leu	Phe	Glu	Asn	Thr	Lys	Ile
	210					215					220				
Asn	Pro	Arg	Asp	Ile	Gly	Val	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn
225					230					235					240
Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	Arg
				245					250					255	
Gly	Asn	Val	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly
			260					265					270		
Val	Ile	Ser	Ile	Asp	Leu	Ala	Lys	Asp	Met	Leu	Gln	Val	His	Arg	Asn
		275					280					285			
Thr	Tyr	Ala	Val	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Asn	Trp	Tyr
	290					295					300				
Phe	Gly	Asn	Lys	Lys	Ala	Met	Leu	Ile	Pro	Asn	Cys	Leu	Phe	Arg	Val
305					310					315					320
Gly	Gly	Ser	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Gly	Lys	Asp	Arg	Arg	Arg
				325					330					335	
Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	Val	Arg	Thr	His	Lys	Gly	Ala	Val
			340					345					350		
Glu	Lys	Ala	Phe	Asn	Cys	Val	Tyr	Gln	Glu	Gln	Asp	Asp	Asn	Gly	Lys
		355					360					365			
Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	Leu	Met	Ala	Ile	Ala	Gly	Glu	Ala
	370					375					380				
Leu	Lys	Ala	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	Ile	Ser
385					390					395					400
Glu	Gln	Ile	Leu	Phe	Met	Thr	Leu	Val	Thr	Lys	Lys	Leu	Phe	Asn	
			405					410						415	
Ser	Lys	Leu	Lys	Pro	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Asp	His
			420					425					430		
Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu	Leu	Glu	Lys
		435					440				445				
Asn	Leu	Gln	Leu	Ser	Gln	Thr	His	Val	Glu	Ala	Ser	Arg	Met	Thr	Leu
	450					455					460				
His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	Glu	Leu	Ala
465					470					475					480
Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Arg	Val	Trp	Gln
				485					490					495	
Ile	Ala	Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	Trp	Val	Ala
			500					505					510		
Leu	Asn	Asn	Val	Lys	Pro	Ser	Val	Ser	Ser	Pro	Trp	Glu	His	Cys	Ile
	515						520					525			
Asp	Arg	Tyr	Pro	Val	Lys	Leu	Asp	Phe							
	530						535								

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCGACGA	TGCCTCAGGC	ACCGATGCCA	GAGTTCTCTA	GCTCGGTGAA	GCTCAAGTAC	60
GTGAAACTTG	GTTACCAATA	TTTGGTTAAC	CATTTCTTGA	GTTTTCTTTT	GATCCCGATC	120
ATGGCTATTG	TCGCCGTTGA	GCTTCTTCGG	ATGGGTCCTG	AAGAGATCCT	TAATGTTTGG	180
AATTCACCTC	AGTTTGACCT	AGTTCAGGTT	CTATGTTCTT	CCTTCTTTGT	CATCTTCATC	240
TCCACTGTTT	ACTTCATGTC	CAAGCCACGC	ACCATCTACC	TCGTTGACTA	TTCTTGTTAC	300
AAGCCACCTG	TCACGTGTCG	TGTCCCCTTC	GCAACTTTCA	TGGAACACTC	TCGTTTGATC	360
CTCAAGGACA	AGCCTAAGAG	CGTCGAGTTC	CAAATGAGAA	TCCTTGAACG	TTCTGGCCTC	420
GGTGAGGAGA	CTTGCTCTCC	TCCGGCTATT	CATTATATTC	CTCCACACAC	AACCATGGAC	480
GCGGCTAGAA	GCGAGGCTCA	GATGGTTATC	TTCCGAGGCCA	TGGACGATCT	TTTCAAGAAA	540
ACCGGTCCTA	AACCTAAAGA	CGTCGACATC	CTTATCGTCA	ACTGCTCTCT	TTTCTCTCCC	600

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ACACCATCGC	TCTCAGCTAT	GGTCATCAAC	AAATATAAGC	TTAGGAGTAA	TATCAAGAGC	660
TTCAATCTTT	CGGGGATGGG	CTGCAGCGCG	GGCCTGATCT	CAGTTGATCT	AGCCCGCGAC	720
TTGCTCCAAG	TTCATCCCAA	TTCAAATGCA	ATCATCGTCA	GCACGGAGAT	CATAACGCCT	780
AATTACTATC	AAGGCAACGA	GAGAGCCATG	TTGTTACCCA	ATTGTCTCTT	CCGCATGGGT	840
GCGGCAGCCA	TACACATGTC	AAACCGCCGG	TCTGACCGGT	GGCGAGCCAA	ATACAAGCTT	900
TCCCACCTCG	TCCGGACACA	CCGTGGCGCT	GACGACAAGT	CTTTCTACTG	TGTCTACGAA	960
CAGGAAGACA	AAGAAGGACA	CGTTGGCATC	AAC TTGTCCA	AAGATCTCAT	GGCCATCGCC	1020
GGTGAAGCCC	TCAAGGCAAA	CATCACCACA	ATAGGTCCTT	TGGTCCTACC	GGCGTCAGAA	1080
CAACTTCTCT	TCCTCACGTC	CCTAATCGGA	CGTAAAATCT	TCAACCCGAA	ATGGAAACCA	1140
TACATACCGG	ATTTCAAGCT	GGCCTTCGAA	CAC TTTTGCA	TTCACGCAGG	AGGCAGAGCG	1200
GTGATCGACG	AGCTCCAAAA	GAATCTACAA	CTATCAGGAG	AACACGTTGA	GGCCTCAAGA	1260
ATGACACTAC	ATCGTTTTGG	TAACACGTCA	TCTTCATCGT	TATGGTACGA	GCTTAGCTAC	1320
ATCGAGTCTA	AAGGGAGAAT	GAGGAGAGGC	GATCGCGTTT	GGCAAATCGC	GTTTGGGAGT	1380
GGTTTCAAGT	GTA ACTCTGC	CGTGTGGAAG	TGTAACCGTA	CGATTAAGAC	ACCTAAGGAC	1440
GGACCATGGT	CCGATTGTAT	CGACCGTTAC	CCTGTCTTTA	TTCCCGAAGT	TGTCAAATCT	1500
TA						1502

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser	Pro	Thr	Met	Pro	Gln	Ala	Pro	Met	Pro	Glu	Phe	Ser	Ser	Ser	Val
1				5					10					15	
Lys	Leu	Lys	Tyr	Val	Lys	Leu	Gly	Tyr	Gln	Tyr	Leu	Val	Asn	His	Phe
			20					25					30		
Leu	Ser	Phe	Leu	Leu	Ile	Pro	Ile	Met	Ala	Ile	Val	Ala	Val	Glu	Leu
			35					40					45		
Leu	Arg	Met	Gly	Pro	Glu	Glu	Ile	Leu	Asn	Val	Trp	Asn	Ser	Leu	Gln
			50				55				60				
Phe	Asp	Leu	Val	Gln	Val	Leu	Cys	Ser	Ser	Phe	Phe	Val	Ile	Phe	Ile
65					70					75					80
Ser	Thr	Val	Tyr	Phe	Met	Ser	Lys	Pro	Arg	Thr	Ile	Tyr	Leu	Val	Asp
					85				90					95	
Tyr	Ser	Cys	Tyr	Lys	Pro	Pro	Val	Thr	Cys	Arg	Val	Pro	Phe	Ala	Thr
			100					105					110		
Phe	Met	Glu	His	Ser	Arg	Leu	Ile	Leu	Lys	Asp	Lys	Pro	Lys	Ser	Val
			115				120					125			
Glu	Phe	Gln	Met	Arg	Ile	Leu	Glu	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr
			130				135				140				
Cys	Leu	Pro	Pro	Ala	Ile	His	Tyr	Ile	Pro	Pro	Thr	Pro	Thr	Met	Asp
145					150				155					160	
Ala	Ala	Arg	Ser	Glu	Ala	Gln	Met	Val	Ile	Phe	Glu	Ala	Met	Asp	Asp
				165					170					175	
Leu	Phe	Lys	Lys	Thr	Gly	Leu	Lys	Pro	Lys	Asp	Val	Asp	Ile	Leu	Ile
			180					185					190		
Val	Asn	Cys	Ser	Leu	Phe	Ser	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val
			195				200					205			
Ile	Asn	Lys	Tyr	Lys	Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Ser
			210				215					220			
Gly	Met	Gly	Cys	Ser	Ala	Gly	Leu	Ile	Ser	Val	Asp	Leu	Ala	Arg	Asp
225					230				235					240	
Leu	Leu	Gln	Val	His	Pro	Asn	Ser	Asn	Ala	Ile	Ile	Val	Ser	Thr	Glu
				245					250					255	
Ile	Ile	Thr	Pro	Asn	Tyr	Tyr	Gln	Gly	Asn	Glu	Arg	Ala	Met	Leu	Leu
			260					265					270		
Pro	Asn	Cys	Leu	Phe	Arg	Met	Gly	Ala	Ala	Ala	Ile	His	Met	Ser	Asn
			275				280					285			
Arg	Arg	Ser	Asp	Arg	Trp	Arg	Ala	Lys	Tyr	Lys	Leu	Ser	His	Leu	Val
			290				295				300				

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Arg Thr His Arg Gly Ala Asp Asp Lys Ser Phe Tyr Cys Val Tyr Glu
305          310          315          320
Gln Glu Asp Lys Glu Gly His Val Gly Ile Asn Leu Ser Lys Asp Leu
          325          330          335
Met Ala Ile Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr Thr Ile Gly
          340          345          350
Pro Leu Val Leu Pro Ala Ser Glu Gln Leu Leu Phe Leu Thr Ser Leu
          355          360          365
Ile Gly Arg Lys Ile Phe Asn Pro Lys Trp Lys Pro Tyr Ile Pro Asp
          370          375          380
Phe Lys Leu Ala Phe Glu His Phe Cys Ile His Ala Gly Gly Arg Ala
385          390          395          400
Val Ile Asp Glu Leu Gln Lys Asn Leu Gln Leu Ser Gly Glu His Val
          405          410          415
Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser
          420          425          430
Ser Leu Trp Tyr Glu Leu Ser Tyr Ile Glu Ser Lys Gly Arg Met Arg
          435          440          445
Arg Gly Asp Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys
          450          455          460
Asn Ser Ala Val Trp Lys Cys Asn Arg Thr Ile Lys Thr Pro Lys Asp
465          470          475          480
Gly Pro Trp Ser Asp Cys Ile Asp Arg Tyr Pro Val Phe Ile Pro Glu
          485          490          495
Val Val Lys Leu
          500

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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ATGGACGGTG CCGGAGAATC ACGACTCGGT GGTGATGGTG GTGGTGATGG TTCTGTTGGA      60
GTTTCAGATCC GACAAACACG GATGCTACCG GATTTTCTCC AGAGCGTGAA TCTCAAGTAT      120
GTGAAATTAG GTTACCATT AATTAACTCA AATCTCTTGA CTCTCTGTTT ATTCCCTCTC      180
GCCGTTGTTA TCTCCGTCGA AGCCTCTCAG ATGAACCCAG ATGATCTCAA ACAGCTCTGG      240
ATCCATCTAC AATACAATCT GGTTAGTATC ATCATCTGTT CAGCGATTCT AGTCTTCGGG      300
TTAACGGTTT ATGTTATGAC CCGACCTAGA CCCGTTTACT TGGTTGATTT CTCTTGTTAT      360
CTCCACCTG ATCATCTCAA AGCTCCTTAC GCTCGGTTCA TGGAACATTC TAGACTCACC      420
GGAGATTTCTG ATGACTCTGC TCTCGAGTTT CAACGCAAGA TCCTTGAGCG TTCTGGTTTA      480
GGGGAAGACA CTTATGTCCC TGAAGCTATG CATTATGTTC CACCGAGAAT TTCAATGGCT      540
GCTGCTAGAG AAGAAGCTGA ACAAGTCATG TTTGGTGCTT TAGATAACCT TTTCGCTAAC      600
ACTAATGTGA AACCAAAGGA TATTGGAATC CTTGTTGTGA ATTGTAGTCT CTTTAATCCA      660
ACTCCTTCGT TATCTGCAAT GATTGTGAAC AAGTATAAGC TTAGAGGTAA CATTAGAAGC      720
TACAATCTAG GCGGTATGGG TTGCAGCGCG GGAGTTATCG CTGTGGATCT TGCTAAAGAC      780
ATGTTGTTGG TACATAGGAA CACTTATGCG GTTGTGTTT CTACTGAGAA CATTACTCAG      840
AATTGGTATT TTGGTAACAA GAAATCGATG TTGATACCGA ACTGCTTGTT TCGAGTTGGT      900
GGCTCTGCGG TTTTGCTATC GAACAAGTCG AGGGACAAGA GACGGTCTAA GTACAGGCTT      960
GTACATGTAG TCAGGACTCA CCGTGAGGCA GATGATAAAG CTTTCCGTTG TGTTTATCAA      1020
GAGCAGGATG ATACAGGGAG AACCGGGGTT TCGTTGTCGA AAGATCTAAT GGCGATTGCA      1080
GGGGAACTC TCAAAACCAA TATCACTACA TTGGGTCCTC TTGTTCTACC GATAAGTGAG      1140
CAGATTCTCT TCTTTATGAC TCTAGTTGTG AAGAAGCTCT TTAACGGTAA AGTGAAACCG      1200
TATATCCCGG ATTTCAAAC TGTCTTCGAG CATTTCTGTA TCCATGCTGG TGGAAGAGCT      1260
GTGATCGATG AGTTAGAGAA GAATCTGCAG CTTTCACCAG TTCATGTCGA GGCTTCGAGG      1320
ATGACTCTTC ATCGATTGG TAACACATCT TCGAGCTCCA TTTGGTATGA ATTCGCTTAC      1380
ATTGAAGCGA AGGGAAGGAT GCGAAGAGGT AATCGTGTGT GGCAAATCGC GTTCGGAAGT      1440
GGATTAAAT GTAATAGCGC GATTGGGAA GCATTAAGGC ATGTGAAACC TTCGAACAAC      1500
AGTCCTTGCG AAGATTGTAT TGACAAGTAT CCGGTAACCT TAAGTTAT      1548

```

(2) INFORMATION FOR SEQ ID NO:14:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Asp	Gly	Ala	Gly	Glu	Ser	Arg	Leu	Gly	Gly	Asp	Gly	Gly	Gly	Asp
1				5					10					15	
Gly	Ser	Val	Gly	Val	Gln	Ile	Arg	Gln	Thr	Arg	Met	Leu	Pro	Asp	Phe
			20					25					30		
Leu	Gln	Ser	Val	Asn	Leu	Lys	Tyr	Val	Lys	Leu	Gly	Tyr	His	Tyr	Leu
		35					40					45			
Ile	Ser	Asn	Leu	Leu	Thr	Leu	Cys	Leu	Phe	Pro	Leu	Ala	Val	Val	Ile
	50					55					60				
Ser	Val	Glu	Ala	Ser	Gln	Met	Asn	Pro	Asp	Asp	Leu	Lys	Gln	Leu	Trp
65					70					75					80
Ile	His	Leu	Gln	Tyr	Asn	Leu	Val	Ser	Ile	Ile	Ile	Cys	Ser	Ala	Ile
			85						90					95	
Leu	Val	Phe	Gly	Leu	Thr	Val	Tyr	Val	Met	Thr	Arg	Pro	Arg	Pro	Val
			100					105					110		
Tyr	Leu	Val	Asp	Phe	Ser	Cys	Tyr	Leu	Pro	Pro	Asp	His	Leu	Lys	Ala
	115						120					125			
Pro	Tyr	Ala	Arg	Phe	Met	Glu	His	Ser	Arg	Leu	Thr	Gly	Asp	Phe	Asp
	130					135					140				
Asp	Ser	Ala	Leu	Glu	Phe	Gln	Arg	Lys	Ile	Leu	Glu	Arg	Ser	Gly	Leu
145					150					155					160
Gly	Glu	Asp	Thr	Tyr	Val	Pro	Glu	Ala	Met	His	Tyr	Val	Pro	Pro	Arg
			165					170						175	
Ile	Ser	Met	Ala	Ala	Ala	Arg	Glu	Glu	Ala	Glu	Gln	Val	Met	Phe	Gly
			180					185					190		
Ala	Leu	Asp	Asn	Leu	Phe	Ala	Asn	Thr	Asn	Val	Lys	Pro	Lys	Asp	Ile
	195						200					205			
Gly	Ile	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu
	210					215					220				
Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Arg	Ser
225					230					235					240
Tyr	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	Val	Ile	Ala	Val	Asp
			245						250					255	
Leu	Ala	Lys	Asp	Met	Leu	Leu	Val	His	Arg	Asn	Thr	Tyr	Ala	Val	Val
			260					265					270		
Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Asn	Trp	Tyr	Phe	Gly	Asn	Lys	Lys
		275					280					285			
Ser	Met	Leu	Ile	Pro	Asn	Cys	Leu	Phe	Arg	Val	Gly	Gly	Ser	Ala	Val
	290					295					300				
Leu	Leu	Ser	Asn	Lys	Ser	Arg	Asp	Lys	Arg	Arg	Ser	Lys	Tyr	Arg	Leu
305					310					315					320
Val	His	Val	Val	Arg	Thr	His	Arg	Gly	Ala	Asp	Asp	Lys	Ala	Phe	Arg
			325						330					335	
Cys	Val	Tyr	Gln	Glu	Gln	Asp	Asp	Thr	Gly	Arg	Thr	Gly	Val	Ser	Leu
			340					345					350		
Ser	Lys	Asp	Leu	Met	Ala	Ile	Ala	Gly	Glu	Thr	Leu	Lys	Thr	Asn	Ile
		355					360					365			
Thr	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	Ile	Ser	Glu	Gln	Ile	Leu	Phe
	370					375						380			
Phe	Met	Thr	Leu	Val	Val	Lys	Lys	Leu	Phe	Asn	Gly	Lys	Val	Lys	Pro
385					390					395					400
Tyr	Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Glu	His	Phe	Cys	Ile	His	Ala
			405						410					415	
Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Gln	Leu	Ser
			420					425					430		
Pro	Val	His	Val	Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg	Phe	Gly	Asn
		435					440						445		

[illegible]

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WHAT IS CLAIMED IS:

1. An isolated polynucleotide encoding a polypeptide having an amino acid sequence selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:2, an amino acid sequence substantially identical to SEQ ID NO:4, an amino acid sequence substantially identical to SEQ ID NO:6, an amino acid sequence substantially identical to SEQ ID NO:8, an amino acid sequence substantially identical to SEQ ID NO:10, an amino acid sequence substantially identical to SEQ ID NO:12, and an amino acid sequence substantially identical to SEQ ID NO:14.
2. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:2.
3. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:4.
4. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:6.
5. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:8.
6. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:10.
7. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:12.
8. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:14.

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9. An isolated polynucleotide, wherein said polynucleotide is selected from the group consisting of:

- a) SEQ ID NO:1;
- b) SEQ ID NO:3;
- c) SEQ ID NO:5;
- d) SEQ ID NO:7;
- e) SEQ ID NO:9;
- f) SEQ ID NO:11;
- g) SEQ ID NO:13;
- h) an RNA analog of SEQ ID NO:1;
- i) an RNA analog of SEQ ID NO:3;
- j) an RNA analog of SEQ ID NO:5;
- k) an RNA analog of SEQ ID NO:7;
- l) an RNA analog of SEQ ID NO:9;
- m) an RNA analog of SEQ ID NO:11;
- n) an RNA analog of SEQ ID NO:13;
- o) a polynucleotide having a nucleic acid sequence complementary to a), b), c), d), e), f), g), h), i), j), k), l), m), or n); and
- p) a nucleic acid fragment of a), b), c), d), e), f), g), h), i), j), k), l), m), n), or o) that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14.

10. An isolated polypeptide having an amino acid sequence selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:2, an amino acid sequence substantially identical to SEQ ID NO:4, an amino acid sequence substantially identical to SEQ ID NO:6, an amino acid sequence substantially identical to SEQ ID NO:8, an amino acid sequence substantially identical to SEQ ID NO:10, an amino acid sequence substantially identical to SEQ ID NO:12, and an

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amino acid sequence substantially identical to SEQ ID NO:14.

11. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:2.

12. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:4.

13. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:6.

14. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:8.

15. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:10.

16. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:12.

17. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:14.

18. A transgenic plant containing a nucleic acid construct comprising a polynucleotide selected from the group consisting of:

- a) SEQ ID NO:1;
- b) SEQ ID NO:3;
- c) SEQ ID NO:5;
- d) SEQ ID NO:7;
- e) SEQ ID NO:9;
- f) SEQ ID NO:11;
- g) SEQ ID NO:13;
- h) an RNA analog of SEQ ID NO:1;

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- i) an RNA analog of SEQ ID NO:3;
- j) an RNA analog of SEQ ID NO:5;
- k) an RNA analog of SEQ ID NO:7;
- l) an RNA analog of SEQ ID NO:9;
- m) an RNA analog of SEQ ID NO:11;
- n) an RNA analog of SEQ ID NO:13;
- o) a polynucleotide having a nucleic acid sequence complementary to a), b), c), d), e), f), g), h), i), j), k), l), m), or n); and
- p) a nucleic acid fragment of a), b), c), d), e), f), g), h), i), j), k), l), m), n), or o) that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14.

19. The plant of claim 18, wherein said construct further comprises a regulatory element operably linked to said polynucleotide.

20. The plant of claim 19, wherein said regulatory element is a tissue-specific promoter.

21. The plant of claim 20, wherein said regulatory element is an epidermal cell-specific promoter.

22. The plant of claim 20, wherein said regulatory element is a seed-specific promoter that is operably linked in sense orientation to said polynucleotide.

23. The plant of claim 22, wherein said plant has altered levels of very long chain fatty acids in seeds compared to the levels in a plant lacking said nucleic acid construct.

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24. A transgenic plant containing a nucleic acid construct comprising a polynucleotide encoding a polypeptide selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:2, an amino acid sequence substantially identical to SEQ ID NO:4, an amino acid sequence substantially identical to SEQ ID NO:6, an amino acid sequence substantially identical to SEQ ID NO:8, an amino acid sequence substantially identical to SEQ ID NO:10, an amino acid sequence substantially identical to SEQ ID NO:12, and an amino acid sequence substantially identical to SEQ ID NO:14.

25. The plant of claim 24, wherein said construct further comprises a regulatory element operably linked to said polynucleotide.

26. The plant of claim 25, wherein said regulatory element is a tissue-specific promoter.

27. The plant of claim 26, wherein said regulatory element is an epidermal cell-specific promoter.

28. The plant of claim 26, wherein said regulatory element is a seed-specific promoter that is operably linked in sense orientation to said polynucleotide.

29. The plant of claim 28, wherein said plant has altered levels of very long chain fatty acids in seeds compared to the levels in a plant lacking said nucleic acid construct.

30. A method of altering the levels of very long chain fatty acids in a plant, comprising the steps of:

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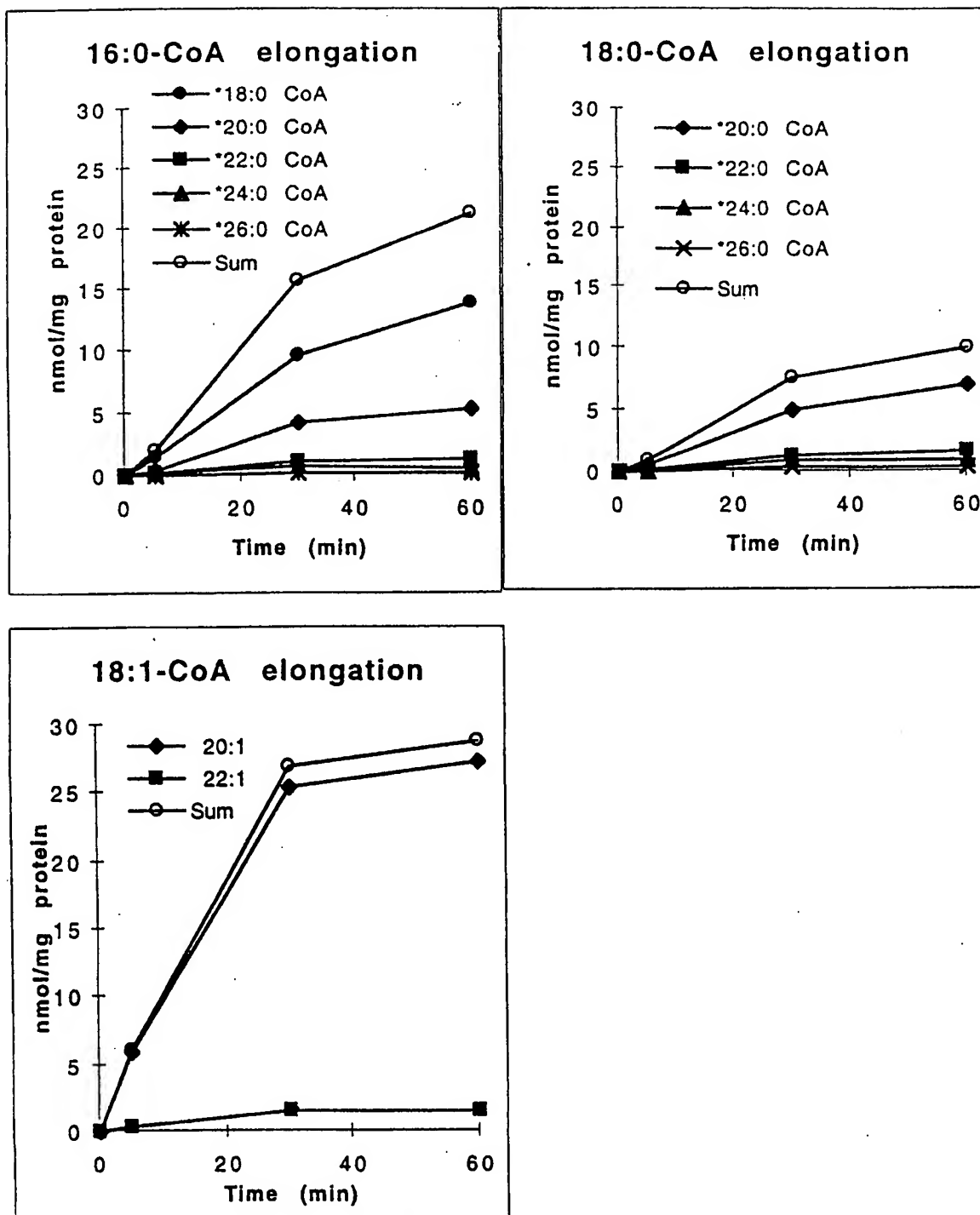
A) creating a nucleic acid construct, said construct comprising a polynucleotide selected from the group consisting of:

- a) SEQ ID NO:1;
 - b) SEQ ID NO:3;
 - c) SEQ ID NO:5;
 - d) SEQ ID NO:7;
 - e) SEQ ID NO:9;
 - f) SEQ ID NO:11;
 - g) SEQ ID NO:13;
 - h) an RNA analog of SEQ ID NO:1;
 - i) an RNA analog of SEQ ID NO:3;
 - j) an RNA analog of SEQ ID NO:5;
 - k) an RNA analog of SEQ ID NO:7;
 - l) an RNA analog of SEQ ID NO:9;
 - m) an RNA analog of SEQ ID NO:11;
 - n) an RNA analog of SEQ ID NO:13;
 - o) a polynucleotide having a nucleic acid sequence complementary to a), b), c), d), e), f), g), h), i), j), k), l), m), or n); and
 - p) a nucleic acid fragment of a), b), c), d), e), f), g), h), i), j), k), l), m), n), or o) that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14; and
- B) introducing said construct into said plant, wherein said polynucleotide is effective for altering the levels of very long chain fatty acids in said plant.

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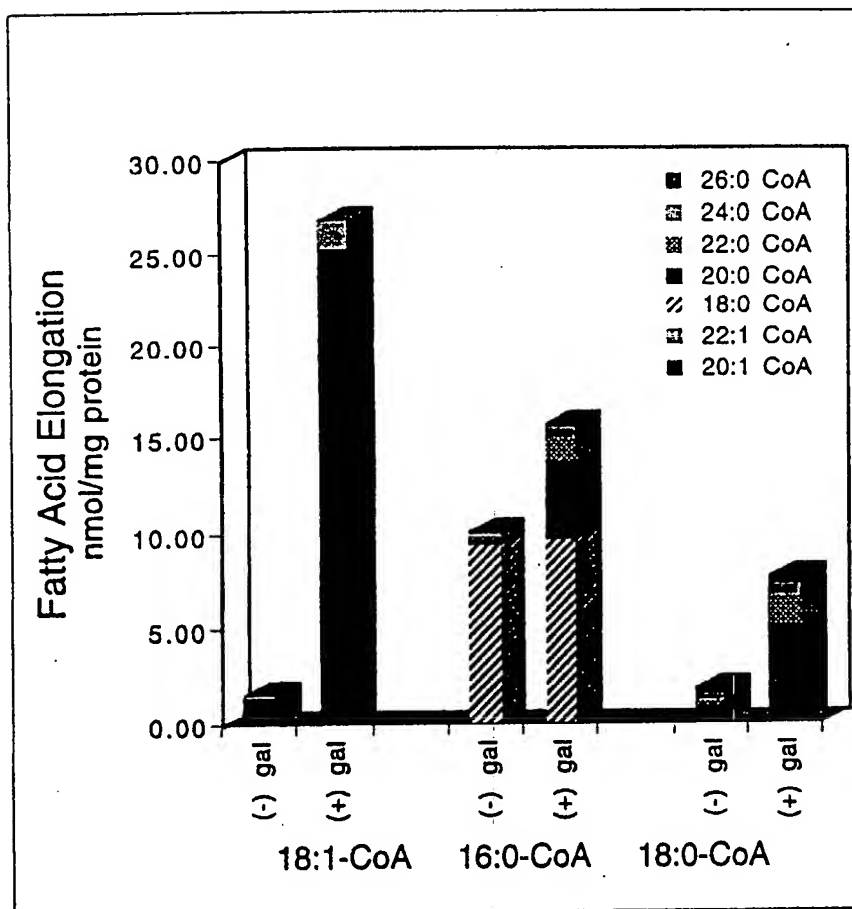
Figure 1

FAE1 w/ respect to time



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Figure 2



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EL1 1560 bases

ATGGATCGAG	AGAGATTAAC	GGCGGAGATG	GCGTTTCGAG	ATTCATCATC	GGCCGTTATA
AGAATTCGAA	GACGTTTGCC	GGATTTATTA	ACGTCCGTTA	AGCTCAAATA	CGTGAAGCCT
GGACTTCACA	ACTCTTGCAA	CGTGACCACC	ATTCTCTTCT	TCTTAATTAT	TCTTCCTTTA
ACCGGAACCG	TGCTGGTTCA	GCTAACCGGT	CTAACGTTTCG	ATACGTTCTC	TGAGCTTTGG
TCTAACCAGG	CGGTTCAACT	CGACACGGCG	ACGAGACTTA	CCTGCTTGGT	TTTCCTCTCC
TTCGTTTTGA	CCCTCTACGT	GGCTAACCGG	TCTAAACCGG	TTTACCTAGT	GGATTTCTCC
TGCTACAAAC	CGGAAGACGA	GCGTAAAATA	TCAGTAGATT	CGTTCTTGAC	GATGACTGAG
GAAAATGGAT	CATTCACCGA	TGACACGGTT	CAGTTCCAGC	AAAGAATCTC	GAACCGGGCC
GGTTTGGGAG	ACGAGACGTA	TCTGCCACGT	GGCATAACTT	CAACGCCCCC	GAAGCTAAAT
ATGTCAGAGG	CACGTGCCGA	AGCTGAAGCC	GTTATGTTTG	GAGCCTTAGA	TTCCCTCTTC
GAGAAAACCG	GAATTAAACC	GGCCGAAGTC	GGAATCTTGA	TAGTAAACTG	CAGCTTATTC
AATCCGACGC	CGTCTCTATC	AGCGATGATC	GTGAACCATT	ACAAGATGAG	AGAAGACATC
AAAAGTTACA	ACCTCGGAGG	AATGGGTTGC	TCCGCCGGAT	TAATCTCAAT	CGATCTCGCT
AACAATCTCC	TCAAAGCAAA	CCCTAATTCT	TACGCTGTCT	TGGTAAGCAC	GGAAAACATA
ACCCTAAACT	GGTACTTCGG	AAATGACCGG	TCAATGCTCC	TCTGCAACTG	CATCTTCCGA
ATGGGCGGAG	CTGCGATTCT	CCTCTCTAAC	CGCCGTCAAG	ACCGGAAGAA	GTCAAAGTAC
TCGCTGGTCA	ACGTCGTTCT	AACACATAAA	GGATCAGACG	ACAAGAATA	CAATTGCGTG
TACCAGAAGG	AAGACGAGAG	AGGAACAATC	GGTGTCTCTT	TAGCTAGAGA	GCTCATGTCT
GTCCGCCGGAG	ACGCTCTGAA	AACAACATC	ACGACTTTAG	GACCGATGGT	TCTTCCATTG
TCAGAGCAGT	TGATGTTCTT	GATTTCTTTG	GTCAAAAGGA	AGATGTTCAA	GTTAAAAGTT
AAACCGTATA	TTCCGGATTT	CAAGCTAGCT	TTCGAGCATT	TCTGTATTCA	CGCAGGAGGT
AGAGCGGTTT	TAGACGAAGT	GCAGAAGAAT	CTTGATCTCA	AAGATTGGCA	CATGGAACCT
TCTAGAATGA	CTTTGCACAG	ATTTGGTAAC	ACTTCGAGTA	GCTCGCTTTG	GTATGAGATG
GCTTATAACCG	AAGCTAAGGG	TCGGGTAA	GCTGGTGACC	GACTTTGGCA	GATTGCGTTT
GGATCGGGTT	TCAAGTGTA	TAGTGCGGTT	TGGAAAGCGT	TACGACCGGT	TTCGACGGAG
GAGATGACCG	GTAATGCTTG	GGCTGCTTCG	ATTGATCAAT	ATCCGGTTAA	AGTTGTGCAA

EL1
FIGURE 3

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EL1 sequence

Molecular Weight 58379.00 Daltons

520 Amino Acids

62 Strongly Basic(+) Amino Acids (K,R)

52 Strongly Acidic(-) Amino Acids (D,E)

187 Hydrophobic Amino Acids (A,I,L,F,W,V)

144 Polar Amino Acids (N,C,Q,S,T,Y)

8.784 Isoelectric Point

10.804 Charge at PH 7.0

MDRERLTAEM	AFRDSSSAVI	RIRRRLPDLL	TSVKLKYYVKL	GLHNSCNVTT	ILFFLIILPL
TGTVLVQLTG	LTFDTFSELW	SNQAVQLDTA	TRLTCLVFLS	FVLTLTYVANR	SKPVYLVDFS
CYKPEDERKI	SVDSFLTMTTE	ENGSTDDTV	QFQQRISNRA	GLGDETYLPR	GITSTPPKLN
MSEARAEAEA	VMFGALDSL	EKTGIKPAEV	GILIVNCSLF	NPTPSLSAMI	VNHYKMREDI
KSYNLGGMGC	SAGLISIDLA	NNLLKANPNS	YAVVVSTENI	TLNWFYGNDR	SMLLCNCIFR
MGGAAILLN	RRQDRKKSKY	SLVNVVRTHK	GSDDKNYNCV	YQKEDERG	GVSLARELMS
VAGDALKTNI	TTLGPMVLPL	SEQLMFLISL	VKRKMFCLKV	KPYIPDFKLA	FEHFCIHAGG
RAVLDEVQKN	LDLKDWHMEP	SRMTLHRFGN	TSSSSLWYEM	AYTEAKGRVK	AGDRLWQIAF
GSGFKCNSAV	WKALRPVSTE	EMTGNAWAGS	IDQYPVKVVQ		

FIGURE 4

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EL2 1479 bases

ATGGATTACC	CCATGAAGAA	GGTAAAAATC	TTTTTCAACT	ACCTCATGGC	GCATCGCTTC	
AAGCTCTGCT	TCTTACCATT	AATGGTTGCT	ATAGCCGTGG	AGGCGTCTCG	TCTTTCCACA	120
CAAGATCTCC	AAAACTTTTA	CCTCTACTTA	CAAAACAACC	ACACATCTCT	AACCATGTTC	
TTCCTTTACC	TCGCTCTCGG	GTCGACTCTT	TACCTCATGA	CCCGGCCCAA	ACCCGTTTAT	240
CTCGTTGACT	TTAGCTGCTA	CCTCCCACCG	TCGCATCTCA	AAGCCAGCAC	CCAGAGGATC	
ATGCAACACG	TAAGGCTTGT	ACGAGAAGCA	GGCGCGTGGA	AGCAAGAGTC	CGATTACTTG	360
ATGGACTTCT	GCGAGAAGAT	TCTAGAACGT	TCCGGTCTAG	GCCAAGAGAC	GTACGTACCC	
GAAGGTCTTC	AAACTTTGCC	ACTACAACAG	AATTTGGCTG	TATCACGTAT	AGAGACGGAG	480
GAAGTTATTA	TTGGTGCGGT	CGATAATCTG	TTTCGCAACA	CGGGAATAAG	CCCTAGTGAT	
ATAGGTATAT	TGGTGGTGAA	TTCAAGCACT	TTTAATCCAA	CACCTTCGCT	ATCAAGTATC	600
TTAGTGAATA	AGTTTAAACT	TAGGGATAAT	ATAAAGAGCT	TGAATCTTGG	TGGGATGGGG	
TGTAGCGCTG	GAGTCATCGC	TATCGATGCG	GCTAAGAGCT	TGTTACAAGT	TCATAGAAAC	720
ACTTATGCTC	TTGTGGTGAG	CACGGAGAAC	ATCACTCAAA	ACTTGTACAT	GGGTAACAAC	
AAATCAATGT	TGGTTACAAA	CTGTTTGTTT	CGTATAGGTG	GGGCCGCGAT	TTTGCTTTCT	840
AACCGGTCTA	TAGATCGTAA	ACGCGCAAAA	TACGAGCTTG	TTCACACCGT	GCGGGTCCAT	
ACCGGAGCAG	ATGACCGATC	CTATGAATGT	GCAACTCAAG	AAGAGGATGA	AGATGGCATA	960
GTTGGGGTTT	CCTTGTCAAA	GAATCTACCA	ATGGTAGCTG	CAAGAACCCT	AAAGATCAAT	
ATCGCAACTT	TGGGTCCGCT	TGTTCTTCCC	ATAAGCGAGA	AGTTTCACTT	CTTTGTGAGG	1080
TTCGTTAAAA	AGAAGTTTCT	CAACCCCAAG	CTAAAGCATT	ACATTCCGGA	TTTCAAGCTC	
GCATTGAGC	ATTTCTGTAT	CCATGCGGGT	GGTAGAGCGC	TAATTGATGA	GATGGAGAAG	1200
AATCTTCATC	TAACTCCACT	AGACGTTGAG	GCTTCAAGAA	TGACATTACA	CAGGTTTGGT	
AATACCTCTT	CGAGCTCCAT	TTGGTACGAG	TTGGCTTACA	CAGAAGCCAA	AGGAAGGATG	1320
ACGAAAGGAG	ATAGGATTTG	GCAGATTGCG	TTGGGGTCAG	GTTTTAAGTG	TAATAGTTCA	
GTTTGGGTGG	CTCTTCGTAA	CGTCAAGCCT	TCTACTAATA	ATCCTTGGA	ACAGTGTCTA	1440
CACAAATATC	CAGTTGAGAT	CGATATAGAT	TTAAAAGAG			

EL2
FIGURE 5

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EL2 protein sequence
Molecular Weight 55799.30 Daltons
493 Amino Acids
55 Strongly Basic(+) Amino Acids (K,R)
46 Strongly Acidic(-) Amino Acids (D,E)
181 Hydrophobic Amino Acids (A,I,L,F,W,V)
134 Polar Amino Acids (N,C,Q,S,T,Y)
8.756 Isoelectric Point
10.995 Charge at PH 7.0

MDYPMKKVKI	FFNYLMAHRF	KLCFLPLMVA	IAVEASRLST	QDLQNFYLYL	QNNHTSLTMF	FLYLALGSTL
YLMTRPKPVY	LVDFSCYLPP	SHLKASTQRI	MQHVRLVREA	GAWKQESDYL	MDFCEKILER	SGLGQETYVP
EGLQTLPLQQ	NLAVSRIETE	EVIIGAVDNL	FRNTGISPSD	IGILVVNSST	FNPTPSLSSI	LVNKFKLRDN
IKSLNLGGMG	CSAGVIAIDA	AKSLLQVHRN	TYALVVSTEN	ITQNLVGMNN	KSMLVTNCLF	RIGGAAILLS
NRSIDRKRAK	YELVHTVRVH	TGADDRSYEC	ATQEEDEDGI	VGVSLSKNLP	MVAARTLKIN	IATLGPLVLP
ISEKFHFFVR	FVKKKFLNPK	LKHYIPDFKL	AFEHFCIHAG	GRALIDEMEK	NLHLTPLDVE	ASRMTLHRFG
NTSSSSIWYE	LAYTEAKGRM	TKGDRIWQIA	LGSGFKCNSS	VWVALRNVKP	STNNPWEQCL	HKYPVEIDID
LKE						

FIGURE 6

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EL3 1512 bases

```
CTACGTCAGG GTAGAACAAA GAGTAAACAC TTAAGCAAAA CAATTTGTCC TACTCTTAGG TTATCTCCAA
TGAAGAACTT AAAGATGGTT TTCTTCAAGA TCCTCTTTAT CTCTTTAATG GCAGGATTAG CCATGAAAGG
ATCTAAGATC AACGTAGAAG ATCTCCAAAA GTTCTCCCTC CACCATACAC AGAACAACCT CCAAACCATA
AGCCTTCTAT TGTTTCTTGT CGTTTTTGTG TGGATCCTCT ACATGTTAAC CCGACCTAAA CCCGTTTACC
TTGTTGATTT CTCCTGCTAC CTTCCACCGT CGCATCTCAA GGTCAGTATC CAAACCCTAA TGGGACACGC
AAGACGTGCA AGAGAAGCAG GCATGTGTTG GAAGAACAAA GAGAGCGACC ATTTAGTTGA CTTCCAGGAG
AAGATTCTTG AACGTTCCGG TCTTGGTCAA GAAACCTACA TCCCCGAGGG TCTTCAGTGC TTCCCACTTC
AGCAAGGCAT GGGTGCTTCA CGTAAAGAGA CGGAAGAAGT AATCTTCGGA GCTCTTGACA ATCTTTTTTCG
CAACACCGGT GTAAAACCTG ATGATATCGG TATATTGGTG GTGAATTCTA GCACGTTTAA TCCAACCTCA
TCACTCGCCT CCATGATTGT GAACAAGTAC AAACCTCAGAG ACAACATCAA GAGTTTGAAT CTTGGAGGGA
TGGGTTGCAG TGCCGGAGTT ATAGCTGTTG ATGTCGCTAA GGGATTACTA CAAGTTCATA GGAACACTTA
TGCTATTGTA GTAAGCACAG AGAACATCAC TCAGAACTTA TACTTGGGGA AAAACAAATC AATGCTAGTC
ACAAACTGTT TGTTCCGCGT TGGTGGTGCT GCGGTTCTGC TTTCAAACAG ATCTAGAGAC CGTAACCGCG
CCAAATACGA GCTTGTTTAC ACCGTACGGA TCCATACCGG ATCAGATGAT AGGTCGTTTCG AATGTGCGAC
ACAAGAAGAG GATGAAGATG GTATAATTGG AGTTACCTTG ACAAAGAATC TACCTATGGT GGCTGCAAGG
ACTCTTAAGA TAAATATCGC AACTTTGGGT CCTCTTGTA TCCATTAAA AGAGAAGCTA GCCTTCTTTA
TTACTTTTGT CAAGAAGAAG TATTTCAAGC CAGAGTTAAG GAATTATACA CCAGATTTCA AGCTTGCCTT
TGAGCATTTT TGTATCCACG CTGGTGGAAG AGCTCTAATA GATGAGCTGG AGAAGAACCT TAAGCTTTCT
CCGTTACACG TAGAGGCGTC AAGAATGACA CTACACAGGT TTGGTAACAC TTCTTCTAGC TCAATCTGGT
ACGAGTTAGC TTATACAGAA GCTAAAGGAA GGATGAAGGA AGGAGATAGG ATTTGGCAGA TTGCTTTGGG
GTCAGGTTTT AAGTGTAACA GTTCAGTATG GGTGGCTCTG CGAGACGTTA AGCCTTCAGC TAACAGTCCA
TGGGAAGACT GTATGGATAG ATATCCGGTT GAGATTGATA TT
```

EL3
FIGURE 7

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EL3 protein sequence

Molecular Weight 56801.10 Daltons

504 Amino Acids

66 Strongly Basic(+) Amino Acids (K,R)

48 Strongly Acidic(-) Amino Acids (D,E)

183 Hydrophobic Amino Acids (A,I,L,F,W,V)

127 Polar Amino Acids (N,C,Q,S,T,Y)

9.315 Isoelectric Point

19.797 Charge at PH 7.0

LRQGRTKSKH LSKTICPTLR LSPMKNLKMY FFKILFISLM AGLAMKGSKI NVEDLQKFSL HHTQNNLQTI
SLLLFLVVFV WILYMLTRPK PVYLVDVFCY LPPSHLKVSI QTLMGHARRA REAGMCWKKNK ESDHLVDFQE
KILERSGLGQ ETYIPEGLQC FPLQQGMGAS RKETEEVIFG ALDNLFRNTG VKPDDIGILV VNSSTFNPTP
SLASMIVNKY KLRDNIKSLN LGGMGCSAGV IAVDVAKGLL QVHRNTYAIV VSTENITQNL YLGKNKSMVLV
TNCLFRVGGG AVLLSNRSRD RNRKYELVH TVRIHTGSDD RSFECATQEE DEDGIIGVTL TKNLPMVAAR
TLKINIATLG PLVLPLKEKL AFFITFVKKK YFKPELRNYT PDFKLAFEHF CIHAGGRALI DELEKNLKLS
PLHVEASRMT LHRFGNTSSS SIWYELAYTE AKGRMKEGDR IWQIALGSGF KCNSSVWVAL RDVKPSANSP
WEDCMDRYPV EIDI

EL3
FIGURE 8

EL4 cDNA 1650 bases

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ATGGGTTAGAT CCAACGAGCA AGATCTGCTC TCTACCGAGA TCGTTAATCG TGGGATCGAA CCATCCGGTC
CTAACGCCGG CTCACCAACG TTCTCGGTTA GGGTCAGGAG ACGTTTGCCT GATTTTCTTC AGTCGGTGAA
CTTGAAGTAC GTGAAACTTG GTTACCACTA CCTCATAAAC CATGCGGTTT ATTTGGCGAC CATACCGGTT
CTTGTGCTGG TTTTGTAGTC TGAGGTTGGG AGTTTAAGCA GAGAAGAGAT TTGGAAGAAG CTTTGGGACT
ATGATCTTGC AACTGTTATC GGATTCTTCG GTGTCTTTGT TTTAACCGCT TGTGTCTACT TCATGTCTCG
TCCTCGCTCT GTTTATCTTA TTGATTTTCG TTGTTACAAG CCCTCCGATG AACACAAGGT GACAAAAGAA
GAGTTCATAG AACTAGCGAG AAAATCAGGG AAGTTCGACG AAGAGACACT CGGTTTCAAG AAGAGGATCT
TACAAGCCTC AGGCATAGGC GACGAGACAT ACGTCCCAAG ATCCATCTCT TCATCAGAAA ACATAACAAC
GATGAAAGAA GGTCGTGAAG AAGCCTCTAC AGTGATCTTT GGAGCACTAG ACGAACTCTT CGAGAAGACA
CGTGTAAGAA CTAAAGACGT TGGTGTCCTT GTGGTTAACT GTAGCATTTT CAACCCGACA CCGTCGTTGT
CCGCAATGGT GATAAACCAT TACAAGATGA GAGGGAACAT ACTTAGTTAC AACCTTGGAG GGATGGGATG
TTCGGCTGGA ATCATAGCTA TTGATCTTGC TCGTGACATG CTTCAGTCTA ACCCTAATAG TTATGCTGTT
GTTGTGAGTA CTGAGATGGT TGGGTATAAT TGGTACGTGG GAAGTGACAA GTCAATGGTT ATACCTAATT
GTTTCTTTAG GATGGGTTGT TCTGCCGTTA TGCTCTCTAA CCGTCGTCGT GACTTTTCGCC ATGCTAAGTA
CCGTCTCGAG CACATTGTCC GAACTCATAA GGCTGCTGAC GACCGTAGCT TCAGGAGTGT GTACCAGGAA
GAAGATGAAC AAGGATTCAA GGGGTGAAG ATAAGTAGAG ACTTAATGGA AGTTGGAGGT GAAGCTCTCA
AGACAAACAT CACTACCTTA GGTCTCTTTG TCCTACCTTT CTCCGAGCAG CTTCTCTTCT TTGCTGCTTT
GGTCCGCCGA ACATTCTCAC CTGCTGCCAA AACGTCCACA ACCACTTCCT TCTCTACTTC CGCCACCGCA
AAAACCAATG GAATCAAGTC TTCCTCTTCC GATCTGTCCA AGCCATACAT CCCGGACTAC AAGCTCGCCT
TCGAGCATTT TTGCTTCCAC GCGGCAAGCA AAGTAGTGCT TGAAGAGCTT CAAAAGAATC TAGGCTTGAG
TGAAGAGAAT ATGGAGGCTT CTAGGATGAC ACTTCACAGG TTTGGAAACA CTTCTAGCAG TGGAATCTGG
TATGAGTTGG CTTACATGGA GGCCAAGGAA AGTGTTTCGT GAGGCGATAG GGTTTGGCAG ATCGCTTTTCG
GTTCTGGTTT TAAGTGTAAC AGTGTGGTGT GGAAGGCAAT GAGGAAGGTG AAGAAGCCAA CCAGGAACAA
TCCTTGGGTG GATTGCATCA ACCGTTACCC TGTGCCTCTC

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EL4
FIGURE 9

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EL4 protein sequence

Molecular Weight 61953.80 Daltons

550 Amino Acids

71 Strongly Basic(+) Amino Acids (K,R)

58 Strongly Acidic(-) Amino Acids (D,E)

191 Hydrophobic Amino Acids (A,I,L,F,W,V)

147 Polar Amino Acids (N,C,Q,S,T,Y)

9.036 Isoelectric Point

14.349 Charge at PH 7.0

MGRSNEQDLL	STEIVNRGIE	PSGPNAGSPT	FSVRVRRRLP	DFLQSVNLKY	VKLGYHYLIN	HAVYLATIPV
LVLVFSAEVG	SLSREEIWKK	LWDYDLATVI	GFFGVFVLTA	CVYFMSRPRS	VYLIDFACYK	PSDEHKVTKE
EFIELARKSG	KFDEETLGFK	KRILQASGIG	DETYVPRISIS	SSENITTMKE	GREEASTVIF	GALDELFEKT
RVKPKDVGVL	VVNCISIFNPT	PSLSAMVINH	YKMRGNILSY	NLGGMGCSAG	IIAIDLARDM	LQSNPNYSYAV
VVSTEMVGYN	WYVGSDKSMV	IPNCFFRMGC	SAVMLSNRRR	DFRHAKYRLE	HIVRTHKAAD	DRSFRSVYQE
EDEQGFKGLK	ISRDLMEVGG	EALKTNITTL	GPLVLPFSEQ	LLFFAALVRR	TFSPAAKTST	TTSFSTSATA
KTINGIKSSSS	DLSKPYIPDY	KLAFEHFCFH	AASKVVLEEL	QKNLGLSEEN	MEASRMTLHR	FGNTSSSGIW
YELAYMEAKE	SVRRGDRVWQ	IAFGSGFKCN	SVVWKAMRKV	KKPTRNNPWV	DCINRYPVPL	

EL4
FIGURE 10

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EL5 cDNA 1611 bases

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TCGAGCTACG TCAGGGCCTTT TATATGCACA AATTCTCATA AAGTTTTCAA TTTTATTCCA TTTTCTCGG
AAGCCATGGA AGCTGCTAAT GAGCCTGTTA ATGGCGGATC CGTACAGATC CGAACAGAGA ACAACGAAAG
ACGAAAGCTT CCTAATTTCT TACAAAGCGT CAACATGAAA TACGTCAAGC TAGGTTATCA TTACCTCATT
ACTCATCTCT TCAAGCTCTG TTTGGTTCCA TTAATGGCGG TTTTAGTCAC AGAGATCTCT CGATTAACAA
CAGACGATCT TTACCAGATT TGGCTTCATC TCCAATACAA TCTCGTTGCT TTCATCTTTC TCTCTGCTTT
AGCTATCTTT GGCTCCACCG TTTACATCAT GAGTCGTCCC AGATCTGTTT ATCTCGTTGA TTA CTCTTGT
TATCTTCCTC CGGAGAGTCT TCAGGTTAAG TATCAGAAGT TTATGGATCA TTCTAAGTTG ATTGAAGATT
TCAATGAGTC ATCTTTAGAG TTTCAGAGGA AGATTCTTGA ACGTTCTGGT TTAGGAGAAG AGACTTATCT
CCCTGAAGCT TTACATTGTA TCCCTCCGAG GCCTACGATG ATGGCGGCTC GTGAGGAATC TGAGCAGGTA
ATGTTTGGTG CTCTTGATAA GCTTTTCGAG AATACCAAGA TTAACCCTAG GGATATTGGT GTGTTGGTTG
TGAATTGTAG CTTGTTTAAT CCTACACCTT CGTTGTCAGC TATGATTGTT AACAAGTATA AGCTTAGAGG
GAATGTAAAG AGTTTAAACC TTGGTGGAAT GGGGTGTAGT GCTGGTGTTA TCTCTATCGA TTTAGCTAAA
GATATGTTGC AAGTTCATAG GAATACTTAT GCTGTTGTGG TTAGTACTGA GAACATTACT CAGAATTGGT
ATTTTGGGAA TAAGAAGGCT ATGTTGATTG CGAATTGTTT GTTTCGTGTT GGTGGTTCGG CGATTTTGTT
GTGCAACAAG GGGAAAGATC GTAGACGGTC TAAGTATAAG CTTGTTTATA CCGTTAGGAC TCATAAAGGA
GCTGTTGAGA AGGCTTTCAA CTGTGTTTAC CAAGAGCAAG ATGATAATGG GAAGACCGGG GTTTCGTTGT
CGAAAGATCT TATGGCTATA GCTGGGGAAG CTCTTAAGGC GAATATCACT ACTTTAGGTC CTTTGGTTCT
TCCTATAAGT GAGCAGATTG TGTTTTTCAT GACTTTGGTT ACGAAGAAAC TGTTTAACTC GAAGCTGAAG
CCGTATATTC CGGATTTCAG GCTTGCGTTT GATCATTCTT GTATCCATGC TGGTGGTAGA GCTGTGATTG
ATGAGCTTGA GAAGAATCTG CAGCTTTTCG AGACTCATGT CGAGGCATCC AGAATGACAC TGCACAGATT
TGGAACACT TCTTCGAGCT CGATTGTTG TGAAGTGGCT TACATAGAGG CTAAAGGTAG GATGAAGAAA
GGAAACCGGG TTTGGCAGAT TGCTTTTGGA AGTGGGTTTA AGTGTAACAG TGCAGTTTGG GTGGCTCTAA
ACAATGTCAA GCCTTCGGTT AGTAGTCCGT GGAACACTG CATCGACCGA TATCCGGTTA AGCTCGACTT
C

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EL5
FIGURE 11

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EL5 protein sequence

Molecular Weight 60874.60 Daltons

537 Amino Acids

63 Strongly Basic(+) Amino Acids (K,R)

47 Strongly Acidic(-) Amino Acids (D,E)

198 Hydrophobic Amino Acids (A,I,L,F,W,V)

148 Polar Amino Acids (N,C,Q,S,T,Y)

9.107 Isoelectric Point

17.930 Charge at PH 7.0

```
SSYVRAFICT NSHKVFNFIP FFSEAMEAAN EPVNGGSVQI RTENNERRKL PNFLQSVNMK YVKLGYYHYLI
THLFKLCCLVP LMAVLVTEIS RLTTDDLYQI WLHLQYNLVA FIFLSALAIF GSTVYIMSRP RSVYLVYDSC
YLPPESLQVK YQKFMDHSKL IEDFNESSLE FQRKILERSG LGEETYLPEA LHCIPPRPTM MAAREESEQV
MFGALDKLFE NTKINPRDIG VLVVNCSLFN PTPSLSAMIV NKYKLRGNVK SFNLGGMGCS AGVISIDLAK
DMLQVHRNTY AVVVSTENIT QNWFYFGNKA MLIPNCLFRV GGSAILLSNK GKDRRRSKYK LVHTVRTHKG
AVEKAFNCVY QEQDDNGKTG VLSKDLMAI AGEALKANIT TLGPLVLPIS EQILFFMTLV TKKLFNSKLG
PYIPDFKLAF DHFCIHAGGR AVIDELEKNL QLSQTHVEAS RMTLHRFGNT SSSSIWYELA YIEAKGRMCK
GNRVWQIAFG SGFKCNSAVW VALNNVKPSV SSPWEHCIDR YPVKLDLF
```

EL5
FIGURE 12

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EL6 1502 bases

TCTCCGACGATGCCTCAGGCACCGATGCCAGAGTTCTCTAGCTCGGTGAAGCTCAAGTACGTGAAACTTGGTTACCAA
TATTTGGTTAACCATTTCTTGAGTTTTCTTTTGATCCCGATCATGGCTATTGTGCGCCGTTGAGCTTCTTCGGATGGGT
CCTGAAGAGATCCTTAATGTTTGAATTCACCTCCAGTTTGACCTAGTTTCAGGTTCTATGTTCTTCTTCTTTGTCTC
TTCATCTCCACTGTTTACTTTCATGTCCAAGCCACGCACCATCTACCTCGTTGACTATTCTTGTTACAAGCCACCTGTC
ACGTGTGCGTGTCCCTTCGCAACTTTCATGGAACACTCTCGTTTGATCCTCAAGGACAAGCCTAAGAGCGTCGAGTTC
CAAATGAGAATCCTTGAACGTTCTGGCCTCGGTGAGGAGACTTGTCTCCCTCCGGCTATTTCATTATATTCCTCCACA
CCAACCATGGACGCGGCTAGAAGCGAGGCTCAGATGGTTATCTTCGAGGCCATGGACGATCTTTTCAAGAAAACCGGT
CTTAAACCTAAAGACGTCGACATCCTTATCGTCAACTGCTCTCTTTTCTCTCCACACCATCGCTCTCAGCTATGGTC
ATCAACAAATATAAGCTTAGGAGTAATATCAAGAGCTTCAATCTTTTCGGGGATGGGCTGCAGCGCGGGCCTGATCTCA
GTTGATCTAGCCCGGACTTGCTCCAAGTTCATCCCAATTCAAATGCAATCATCGTCAGCACGGAGATCATAACGCCT
AATTACTATCAAGGCAACGAGAGAGCCATGTTGTTACCCAATTGTCTCTTCCGCATGGGTGCGGCAGCCATACACATG
TCAAACCGCCGGTCTGACCGGTGGCGAGCCAAATACAAGCTTTCCACCTCGTCCGGACACACCGTGGCGCTGACGAC
AAGTCTTTCTACTGTGTCTACGAACAGGAAGACAAAGAAGGACACGTTGGCATCAACTTGTCCAAAGATCTCATGGCC
ATCGCCGGTGAAGCCCTCAAGGCAAACATCACCACAATAGGTCCTTTGGTCCTACCGCGCTCAGAACAACCTTCTCTTC
CTCAGCTCCCTAATCGGACGTAAAACTTCAACCCGAAATGGAAACCATACATACCGGATTTCAAGCTGGCCTTCGAA
CACTTTTGCATTACGCAGGAGGCAGAGCGGTGATCGACGAGCTCCAAAAGAATCTACAACATATCAGGAGAACACGTT
GAGGCCTCAAGAATGACACTACATCGTTTTGGTAACACGTCATCTTCATCGTTATGGTACGAGCTTAGCTACATCGAG
TCTAAAGGGAGAATGAGGAGAGGCGATCGCGTTTGGCAAATCGCGTTTGGGAGTGGTTTCAAGTGTAACCTCTGCCGTG
TGGAAGTGTAACCGTACGATTAAGACACCTAAGGACGGACCATGGTCCGATTGTATCGACCGTTACCCTGTCTTTATT
CCCGAAGTTGTCAAACCTCA

EL6
FIGURE 13

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EL6 protein sequence

Molecular Weight 56687.90 Daltons

500 Amino Acids

59 Strongly Basic(+) Amino Acids (K,R)

46 Strongly Acidic(-) Amino Acids (D,E)

182 Hydrophobic Amino Acids (A,I,L,F,W,V)

127 Polar Amino Acids (N,C,Q,S,T,Y)

8.909 Isoelectric Point

14.567 Charge at PH 7.0

SPTMPQAPMP EFSSSVKLKY VKLGYQYLVN HFLSFLLIPI MAIVAVELLR MGPEEILNVW NSLQFDLVQV
LCSSFFVIFI STVYFMSKPR TIYLVYDSCY KPPVTCRVPE ATFMHSRLI LKDKPKSVEF QMRILERSGL
GEETCLPPAI HYIPPTPTMD AARSEAQMPI FEAMDDLFFK TGLKPKDVIDI LIVNCSLFSP TPLSAMVIN
KYKLRSNIKS FNLSGMGCSA GLISVDLARD LLQVHPNSNA IIVSTEIITP NYYQGNERAM LLPNCLFRMG
AAAIHMSNRR SDRWRKYKL SHLVRTHRGA DDKSFYCVYE QEDKEGHVGI NLSKDLMAIA GEALKANITT
IGPLVLPASE QLLFLTSLIG RKIFNPKWKP YIPDFKLAFE HFCIHAGGRA VIDELQKNLQ LSGEHVEASR
MTLHRFGNTS SSSLWYELSY IESKGRMRRG DRVWQIAFGS GFKCNSAVWK CNRTIKTPKD GPWSDCIDRY
PVFIPEVVKL

EL6
FIGURE 14

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EL7 1548 bases

ATGGACGGTGCCGGAGAATCACGACTCGGTGGTGATGGTGGTGGTGGTGGTCTGTTGGAGTTCAGATCCGACAAACA
CGGATGCTACCGGATTTTCTCCAGAGCGTGAATCTCAAGTATGTGAAATTAGGTTACCATTACTTAATCTCAAATCTC
TTGACTCTCTGTTTATTCCCTCTCGCCGTTGTTATCTCCGTCGAAGCCTCTCAGATGAACCCAGATGATCTCAAACAG
CTCTGGATCCATCTACAATAACAATCTGGTTAGTATCATCATCTGTTTCAGCGATTCTAGTCTTCGGGTTAACGGTTTAT
GTTATGACCCGACCTAGACCCGTTTACTTGGTTGATTTCTCTTGGTTATCTCCACCTGATCATCTCAAAGCTCCTTAC
GCTCGGTTTCATGGAACATTCTAGACTCACCGGAGATTTGATGACTCTGCTCTCGAGTTTCAACGCAAGATCCTTGAG
CGTTCTGGTTTATAGGGGAAGACACTTATGTCCCTGAAGCTATGCATTATGTTCCACCGAGAATTTCAATGGCTGCTGCT
AGAGAAGAAGCTGAACAAGTCATGTTTGGTGCTTTAGATAACCTTTTCGCTAACACTAATGTGAAACCAAAGGATATT
GGAATCCTTGTTGTGAATTGTAGTCTCTTAAATCCAACCTCCTTCGTTATCTGCAATGATTGTGAACAAGTATAAGCTT
AGAGGTAACATTAGAAGCTACAATCTAGGCGGTATGGGTTGCAGCGCGGGAGTTATCGCTGTGGATCTTGCTAAAGAC
ATGTTGTTGGTACATAGGAACACTTATGCGGTTGTTGTTTCTACTGAGAACATTACTCAGAATTGGTATTTTGGTAAC
AAGAAATCGATGTTGATAACCGAAGTCTTGTTCGAGTTGGTGGCTCTGCGGTTTTGCTATCGAACAAGTCGAGGGAC
AAGAGACGGTCTAAGTACAGGCTTGATCATGTAGTCAGGACTCACCGTGGAGCAGATGATAAAGCTTTCCGTTGTGTT
TATCAAGAGCAGGATGATACAGGGAGAACCGGGGTTTTGTTGTCGAAAGATCTAATGGCGATTGCAGGGGAAACTCTC
AAAACCAATATCACTACATTGGGTCCTCTTGTCTACCGATAAGTGAGCAGATTCTCTTCTTTATGACTCTAGTTGTG
AAGAAGCTCTTTAACGGTAAAGTGAAACCGTATATCCCGGATTTCAAACCTTGCTTTTCGAGCATTCTGTATCCATGCT
GGTGGAAGAGCTGTGATCGATGAGTTAGAGAAGAATCTGCAGCTTTACCAAGTTTCATGTCGAGGCTTCGAGGATGACT
CTTCATCGATTTGGTAACACATCTTCGAGCTCCATTTGGTATGAATTGGCTTACATTGAAGCGAAGGGGAAGGATGCGA
AGAGGTAATCGTGTGTTGGCAAATCGCGTTCGGAAGTGGATTTAAATGTAATAGCGCGATTGGGAAGCATTAAAGGCAT
GTGAAACCTTCGAACAACAGTCCTTGGAAGATTGTATTGACAAGTATCCGGTAACCTTAAAGTTAT

EL7
FIGURE 15

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EL7 protein sequence

Molecular Weight 57848.80 Daltons

516 Amino Acids

59 Strongly Basic(+) Amino Acids (K,R)

48 Strongly Acidic(-) Amino Acids (D,E)

189 Hydrophobic Amino Acids (A,I,L,F,W,V)

131 Polar Amino Acids (N,C,Q,S,T,Y)

8.872 Isoelectric Point

12.792 Charge at PH 7.0

MDGAGESRLG GDGGGDGSVG VQIRQTRMLP DFLQSVNLKY VKLGYHYLIS NLLTLCLFPL AVVISVEASQ
MNPDDLKQLW IHLQYNLVS IICSAILVFG LTVYVMTRPR PVYLVDFSCY LPPDHLKAPY ARFMEHSRLT
GDFDDSALEF QRKILERSGL GEDTYVPEAM HYVPPRISMA AAREEAEQVM FGALDNLFAN TNVKPKDIGI
LVVNCSLFNP TPSLSAMIVN KYKLRGNIRS YNLGGMGCSA GVIAVDLAKD MLLVHRNTYA VVVSTENITQ
NWYFGNKKSM LIPNCLFRVG GSAVLLSNKS RDKRRSKYRL VHVVTRHGA DDKAFRCVYQ EQDDTGRTGV
SLSKDLMAIA GETLKTNITT LGPLVLPIS QILFFMTLVV KKLFGNKVKP YIPDFKLAFE HFCIHAGGRA
VIDELEKNLQ LSPVHVEASR MTLHRFGNTS SSSIWYELAY IEAKGRMRRG NRWVQIAFGS GFKCNSAIWE
ALRHVKPSNN SPWEDCIDKY PVTLSY

EL7
FIGURE 16

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/11384

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :AO1H 5/00, C07H 21/00; C12N 15/00, 15/82

US CL :800/205; 435/172.3; 536/23.6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 800/205; 435/172.3; 536/23.6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X - Y	WO 95/15387 A2 (CALGENE INC.) 08 June 1995, especially pages 57-71.	1,9,10,18-20,22-26, 28-30 ----- 2-8,11-17,21,27
X - Y	WO 96/13582 A2 (DNA PLANT TECHNOLOGY CORP.) 09 May 1996, especially pages 33-38.	1,9,10,18,19,24,25 ----- 2-8,11-17,20-23,26-30



Further documents are listed in the continuation of Box C.



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Date of the actual completion of the international search

07 AUGUST 1998

Date of mailing of the international search report

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/11384

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X - Y	JAMES et al. Directed Tagging of the Arabidopsis FATTY ACID ELONGATION1 (FAE1) Gene with the Maize Transposon Activator. The Plant Cell. March 1995, Vol. 7, pages 309-319, see especially pages 316-317.	1,9,10 ----- 2-8,11,17-30